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OM protein - nucleic search, using frame_plus_p2n model

Run on:         October  9, 2002, 17:55:09 ; Search time 230 Seconds
                                             (without alignments)
                                             6009.201 Million cell updates/sec

Title:          US-09-635-501-2
Perfect score:  4291
Sequence:       1 MSSSSWLLLSLVAVTAAQST..........ISKGENNPGFQNTDDVQTSF 805

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters:      3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09635501/runat_09102002_094528_18514/app_query.fasta_1.967
-DB=N_Geneseq_032802 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09635501_@CGN_1_1_70_@runat_09102002_094528_18514 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      N_Geneseq_032802:*
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                23:  /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*
                24:  /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4291	100.0	2418	21	AAZ59465	Human MPROT15 codi
2	4291	100.0	3334	22	AAC84366	Human Zace2 protei
3	4291	100.0	3396	21	AAA12764	cDNA encoding a hu
4	4291	100.0	3396	22	AAD02758	Human angiotensin
5	4142	96.5	3732	22	AAS21279	Human cDNA sequenc
6	4061	94.6	2920	22	AAS14880	Human cDNA encodin
7	4013	93.5	2911	22	AAS14890	Human cDNA encodin
8	3740.5	87.2	2262	21	AAZ59466	Human MPROT15 codi
9	3579	83.4	2638	22	AAC84368	Mouse Zace2-5 prot
10	3561	83.0	2638	22	AAC84370	Mouse Zace2-10 pro
11	3509	81.8	2415	22	AAC84367	Human Zace2 protei
12	3119	72.7	3474	22	AAS42515	Human cDNA encodin
13	2899	67.6	2415	22	AAC84369	Mouse Zace2-5 prot
14	1344	31.3	2477	12	AAQ10328	Encodes human test
15	1337	31.2	4020	21	AAA38330	Human angiotensin-
16	1337	31.2	4024	11	AAQ04027	Human angiotensin
17	1337	31.2	4024	20	AAX35850	Human angiotensin
18	1336	31.1	4020	19	AAV41320	Human angiotensin
19	1334	31.1	3939	22	AAS06085	Angiotensin conver
20	1334	31.1	4563	22	AAS06057	Angiotensin conver
21	1310	30.5	3942	20	AAX35851	Rat angiotensin co
22	1275	29.7	5005	22	AAH57430	Human intestine ce
23	1086	25.3	2089	23	ABL14379	Drosophila melanog
24	1057	24.6	2074	16	AAQ82948	Tick carboxypeptid
25	1028	24.0	2450	23	ABL16697	Drosophila melanog
c 26	961	22.4	9006	22	AAH77873	Nucleotide sequenc
27	941.5	21.9	5632	23	ABL14378	Drosophila melanog
28	919.5	21.4	5060	23	ABL16696	Drosophila melanog
29	721	16.8	2082	21	AAA46692	Degenerate sequenc
30	721	16.8	2082	22	AAS14169	Human zinc metallo
31	715.5	16.7	1395	22	AAH77876	Nucleotide sequenc
32	502.5	11.7	2025	23	ABL04671	Drosophila melanog
33	478	11.1	313	20	AAV86528	EST clone AU47. H
34	476	11.1	1836	23	ABL27143	Drosophila melanog
35	469	10.9	467	19	AAV09277	Nucleotide sequenc
36	445	10.4	5116	23	ABL04670	Drosophila melanog
37	444	10.3	4001	23	ABL27142	Drosophila melanog
38	414.5	9.7	2046	23	ABL05359	Drosophila melanog
39	387	9.0	666	22	AAF94460	Human hydrophobic
40	387	9.0	1347	22	AAF94470	Human hydrophobic
41	384	8.9	1401	19	AAV40540	Homo sapiens secre
42	383	8.9	847	20	AAX30083	Human secreted pro
43	381	8.9	848	20	AAZ40770	Secreted protein e
44	381	8.9	848	20	AAX88191	Human secreted pro
45	381	8.9	848	20	AAX97564	Extended human sec

ALIGNMENTS

```
RESULT 1
AAZ59465
ID   AAZ59465 standard; DNA; 2418 BP.
XX
AC   AAZ59465;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human MPROT15 coding sequence #1.
XX
KW   MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;
KW   heart disease; apoplexy; heart disease; nervous denaturation; ds;
KW   Alzheimer's disease; hormone; cytokine.
XX
OS   Homo sapiens.
XX
PN   JP11318472-A.
XX
```

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PD   24-NOV-1999.
XX
PF   22-JAN-1999;    99JP-0014949.
XX
PR   13-MAY-1998;    98GB-0010373.
PR   18-AUG-1998;    98GB-0018009.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
DR   WPI; 2000-109268/10.
DR   P-PSDB; AAY67310.
XX
PT   MPROT15 polypeptide and MPROT15 polynucleotides - useful for the
PT   treatment of hypertension, myocardial diseases, apoplexy, heart
PT   diseases, nervous denaturation, Alzheimer's disease etc.
XX
PS   Claim 7; Page 14; 22pp; Japanese.
XX
CC   This is the coding sequence of human MPROT15. The MPROT15 polynucleotide
CC   and polypeptide sequences can be used for the treatment of hypertension,
CC   myocardial diseases, apoplexy, heart diseases, nervous denaturation,
CC   Alzheimer's disease and diseases related to the processing of peptide
CC   hormones and cytokines.
XX
SQ   Sequence 2418 BP; 744 A; 484 C; 555 G; 635 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          2418
Score:                    4291.00        Matches:         805
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       21             Gaps:            0

US-09-635-501-2 (1-805) x AAZ59465 (1-2418)

Qy          1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 60

Qy         21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 120

Qy         41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA 180

Qy         61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC 240

Qy         81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTT 300

Qy        101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCAAAATGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTA 360

Qy        121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA 420

Qy        141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAG 480

Qy        161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT 540

Qy        181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGG 600

Qy        201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GATTATTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC 660

Qy        221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT 720

Qy        241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGA 780

Qy        261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCT 840

Qy        281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG 900

Qy        301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT 960

Qy        321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG 1020

Qy        341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG 1080

Qy        361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAG 1140

Qy        381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC 1200

Qy        401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCC 1260

Qy        421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATTGGTCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTC 1320

Qy        441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGG 1380

Qy        461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATG 1440

Qy        481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAGCGAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCC 1500

Qy        501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCATCTCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTT 1560

Qy        521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TACCAATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCAC 1620

Qy        541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1621 AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTT 1680

Qy    561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGAAAATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAAT 1740

Qy    581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAG 1800

Qy    601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AATTCTTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTG 1860

Qy    621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGGATAAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATG 1920

Qy    641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAAT 1980

Qy    661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGATGATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCC 2040

Qy    681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTT 2100

Qy    701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAC 2160

Qy    721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCCTAGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCC 2220

Qy    741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 ATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTG 2280

Qy    761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATCTTCACTGGGATCAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCT 2340

Qy    781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TATGCCTCCATCGATATTAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGAT 2400

Qy    801 ValGlnThrSerPhe 805
          |||||||||||||||
Db   2401 GTTCAGACCTCCTTT 2415

RESULT 2
AAC84366
ID   AAC84366 standard; cDNA; 3334 BP.
XX
AC   AAC84366;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human Zace2 protein encoding cDNA.
XX
KW   Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
KW   zinc metallopeptidase; blood pressure; zinc protease; hypertension;
KW   ventricular systolic dysfunction; renal impairment; heart failure;
KW   scleroderma renal crisis; atherosclerosis;. antiinflammatory; human;
KW   antiarthritic; bradykinin inactivator; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             35..2452
FT                   /*tag= a
FT                   /product= "Zace2"
XX
PN   WO200070032-A1.
XX
PD   23-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US11932.
XX
PR   13-MAY-1999;   99US-0311482.
PR   27-AUG-1999;   99US-0384706.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Piddington CS,  Petrie CR,  Shoemaker KE,  Bishop PD;
XX
DR   WPI; 2001-025018/03.
DR   P-PSDB; AAB48095.
XX
PT   Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
PT   bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
PT   associated with inflammation such as arthritis and enterocolitis -
XX
PS   Example 1; Page 95-100; 125pp; English.
XX
CC   The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
CC   converting enzyme is a zinc metallopeptidase that plays roles in blood
CC   pressure regulation and fertility. Zace2 can be expressed by standard
CC   recombinant methodology. Zace2 polypeptides are useful for treating an
CC   inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
CC   diseases associated with inflammation like arthritis and enterocolitis,
CC   as targets for identifying modulators of zinc protease activity, for
CC   screening or identifying new angiotensin-converting enzyme (ACE)
CC   inhibitors, and as a basis for rational drug design for inhibitory
CC   molecules. The nucleic acids can be used to detect the expression of a
CC   Zace2 gene in a biological sample, as probes for in vivo diagnosis and
CC   for detecting and localizing Zace2 gene expression in tissue samples,
CC   to determine whether a subject's chromosomes contain a mutation in the
CC   Zace2 gene, and to detect aberrations associated with the Zace2 locus.
CC   Inhibitors of ACE are used for treating hypertension of various
CC   conditions, including left ventricular systolic dysfunction, progressive
CC   renal impairment, scleroderma renal crisis, congestive heart failure due
CC   to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
CC   used to treat infertility while Zace2 antagonists are used for inducing
CC   infertility. The present sequence represents a cDNA encoding the human
CC   Zace2 protein.
XX
SQ   Sequence 3334 BP; 1011 A; 640 C; 754 G; 929 T; 0 other;

Alignment Scores:
Pred. No.:              0            Length:         3334
Score:                  4291.00      Matches:        805
Percent Similarity:     100.00%      Conservative:   0
Best Local Similarity:  100.00%      Mismatches:     0
Query Match:            100.00%      Indels:         0
DB:                     22           Gaps:           0

US-09-635-501-2 (1-805) x AAC84366 (1-3334)

Qy      1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     35 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 94

Qy     21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     95 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 154

Qy     41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    155 TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA 214

Qy     61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC 274

Qy         81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTT 334

Qy        101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 CAGCAAAATGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTA 394

Qy        121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA 454

Qy        141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 TGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAG 514

Qy        161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT 574

Qy        181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGG 634

Qy        201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 GATTATTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC 694

Qy        221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 CAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT 754

Qy        241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 CATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGA 814

Qy        261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCT 874

Qy        281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 TTGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG 934

Qy        301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        935 GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT 994

Qy        321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        995 CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG 1054

Qy        341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1055 AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG 1114

Qy        361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1115 TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAG 1174

Qy        381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1175 TATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC 1234

Qy        401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1235 CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCC 1294

Qy        421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1295 ATTGGTCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTC 1354

Qy        441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1355 AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGG 1414

Qy        461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1415 TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATG 1474

Qy        481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1475 AAGCGAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCC 1534

Qy        501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1535 GCATCTCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTT 1594

Qy        521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1595 TACCAATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCAC 1654

Qy        541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1655 AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTT 1714

Qy        561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1715 GGAAAATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAAT 1774

Qy        581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1775 GTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAG 1834

Qy        601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1835 AATTCTTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTG 1894

Qy        621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1895 AGGATAAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATG 1954

Qy        641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1955 TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAAT 2014

Qy        661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2015 CAGATGATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCC 2074

Qy        681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2075 TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTT 2134

Qy        701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2135 GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAC 2194

Qy        721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2195 AGCCTAGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCC 2254

Qy        741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2255 ATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTG 2314

Qy        761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2315 ATCTTCACTGGGATCAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCT 2374

Qy        781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2375 TATGCCTCCATCGATATTAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGAT 2434
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Qy     801 ValGlnThrSerPhe 805
           |||||||||||||||
Db    2435 GTTCAGACCTCCTTT 2449

RESULT 3
AAA12764
ID   AAA12764 standard; cDNA; 3396 BP.
XX
AC   AAA12764;
XX
DT   25-JUL-2000  (first entry)
XX
DE   cDNA encoding a human angiotensin converting enzyme-2 (ACE-2).
XX
KW   Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW   blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW   chronic heart failure; acute heart failure; myocardial infarction;
KW   renal failure; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             82..2499
FT                   /*tag= a
FT                   /product= "angiotensin converting enzyme-2"
FT   sig_peptide     82..135
FT                   /*tag= b
XX
PN   WO200018899-A2.
XX
PD   06-APR-2000.
XX
PF   29-SEP-1999;   99WO-US22976.
XX
PR   30-SEP-1998;   98US-0163648.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton LS,  Robison KE,  Hsieh FY;
XX
DR   WPI; 2000-293140/25.
DR   P-PSDB; AAY84562.
XX
PT   Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT   polypeptide useful for detecting an ACE-2 therapeutic for treating
PT   hypertension, congestive heart failure, myocardial infarction,
PT   atherosclerosis and renal failure -
XX
PS   Claim 1; Fig 1; 138pp; English.
XX
CC   The present sequence encodes a human angiotensin converting enzyme-2
CC   (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
CC   sequence of the full length ACE-2 cDNA was determined from a clone
CC   obtained from a cDNA library prepared from mRNA of a human heart of
CC   a subject who had congestive heart failure. ACE-2 has significant
CC   sequence homologies with ACE enzymes, and has also been shown to
CC   hydrolyse angiotensin I into Ang.(1-9). The ACE-2 therapeutics are
CC   used to treat blood pressure related diseases and conditions, such as
CC   hypertension, congestive heart failure, chronic heart failure, acute
CC   heart failure, myocardial infarction, atherosclerosis and renal
CC   failure.
XX
SQ   Sequence 3396 BP; 1034 A; 660 C; 771 G; 931 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:        3396
Score:                  4291.00        Matches:       805
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     21             Gaps:          0

US-09-635-501-2 (1-805) x AAA12764 (1-3396)

Qy       1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 141

Qy      21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     142 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 201

Qy      41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     202 TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA 261

Qy      61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     262 AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC 321

Qy      81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     322 CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTT 381

Qy     101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     382 CAGCAAAATGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTA 441

Qy     121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     442 AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA 501

Qy     141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     502 TGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAG 561

Qy     161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     562 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT 621

Qy     181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     622 GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGG 681

Qy     201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     682 GATTATTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC 741

Qy     221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     742 CAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT 801

Qy     241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     802 CATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGA 861

Qy     261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     862 TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCT 921

Qy     281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     922 TTGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG 981

Qy     301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     982 GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT 1041

Qy     321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1042 CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG 1101

Qy     341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1102 AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG 1161
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Qy    361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1162 TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAG 1221

Qy    381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1222 TATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC 1281

Qy    401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1282 CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCC 1341

Qy    421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1342 ATTGGTCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTC 1401

Qy    441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1402 AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGG 1461

Qy    461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1462 TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATG 1521

Qy    481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1522 AAGCGAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCC 1581

Qy    501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1582 GCATCTCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTT 1641

Qy    521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1642 TACCAATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCAC 1701

Qy    541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1702 AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTT 1761

Qy    561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1762 GGAAAATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAAT 1821

Qy    581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1822 GTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAG 1881

Qy    601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1882 AATTCTTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTG 1941

Qy    621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1942 AGGATAAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATG 2001

Qy    641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2002 TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAAT 2061

Qy    661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2062 CAGATGATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCC 2121

Qy    681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2122 TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTT 2181

Qy    701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2182 GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAC 2241

Qy    721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 AGCCTAGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCC 2301

Qy    741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 ATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTG 2361

Qy    761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2362 ATCTTCACTGGGATCAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCT 2421

Qy    781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2422 TATGCCTCCATCGATATTAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGAT 2481

Qy    801 ValGlnThrSerPhe 805
          |||||||||||||||
Db   2482 GTTCAGACCTCCTTT 2496
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```
RESULT 4
AAD02758
ID   AAD02758 standard; cDNA; 3396 BP.
XX
AC   AAD02758;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Human angiotensin converting enzyme-2 (ACE-2) cDNA.
XX
KW   Human; angiotensin converting enzyme-2; ACE-2; peptidyl dipeptidase A;
KW   screening; therapy; hypertension; congestive heart failure; CHF;
KW   inflammation; pain; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             82..2499
FT                   /*tag= a
FT                   /product= "Human angiotensin converting enzyme-2
FT                   (ACE-2)"
FT                   /EC_number= "3.4.15.1"
FT                   /note= "This region is referred as SEQ.ID.NO.3 and is
FT                   specifically claimed in claim 26"
FT   sig_peptide     82..135
FT                   /*tag= b
FT   mat_peptide     136..2496
FT                   /*tag= c
FT                   /product= "Human mature angiotensin converting enzyme-2
FT                   (ACE-2)"
XX
PN   US6194556-B1.
XX
PD   27-FEB-2001.
XX
PF   11-DEC-1997;   97US-0989299.
XX
PR   11-DEC-1997;   97US-0989299.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton SL,  Robison KE;
XX
DR   WPI; 2001-210604/21.
DR   P-PSDB; AAY72667.
XX
PT   Novel genes encoding angiotensin converting enzyme-2 useful as
PT   antisense or antigene agents for therapeutics, diagnostics and
PT   screening assays -
XX
PS   Claim 1; Fig 1; 76pp; English.
XX
CC   The present sequence is human angiotensin converting enzyme-2 (ACE-2)
```

```
CC   cDNA. ACE is also referred as peptidyl dipeptidase A. Nucleic acid
CC   sequence encoding ACE-2 is useful as antisense or antigene agents for
CC   sequence specific modulation of gene expression or in the analysis of
CC   single base-pair mutations in the gene. Nucleic acid sequence encoding
CC   ACE-2 is useful in therapeutics, diagnostics and in screening assays.
CC   ACE-2 antagonist is used to treat hypertension or congestive heart
CC   failure (CHF). ACE agonist is used to reduce the inflammation and pain
CC   resulting from an insect sting or bite, which was accompanied by an
CC   injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2
CC   protein levels for determining the disease or condition associated with
CC   an aberrant protein level.
XX
SQ   Sequence 3396 BP; 1034 A; 659 C; 772 G; 931 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:        3396
Score:                  4291.00        Matches:       805
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     22             Gaps:          0

US-09-635-501-2 (1-805) x AAD02758 (1-3396)

Qy        1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       82 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 141

Qy       21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      142 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 201

Qy       41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      202 TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA 261

Qy       61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      262 AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC 321

Qy       81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      322 CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTT 381

Qy      101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      382 CAGCAAAATGGGTCTTCAGTGCTGTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTA 441

Qy      121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      442 AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA 501

Qy      141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      502 TGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAG 561

Qy      161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      562 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT 621

Qy      181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      622 GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGG 681

Qy      201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      682 GATTATTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC 741

Qy      221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      742 CAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT 801

Qy      241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      802 CATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGA 861

Qy      261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      862 TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCT 921

Qy      281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      922 TTGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG 981

Qy      301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      982 GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT 1041

Qy      321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1042 CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG 1101

Qy      341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1102 AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG 1161

Qy      361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1162 TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAG 1221

Qy      381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1222 TATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC 1281

Qy      401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1282 CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCC 1341

Qy      421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1342 ATTGGTCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTC 1401

Qy      441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1402 AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGG 1461

Qy      461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1462 TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATG 1521

Qy      481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
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Db     1522 AAGCGAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCC 1581

Qy      501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
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Db     1582 GCATCTCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTT 1641

Qy      521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
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Db     1642 TACCAATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCAC 1701

Qy      541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
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Db     1702 AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTT 1761

Qy      561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1762 GGAAAATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAAT 1821

Qy      581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1822 GTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAG 1881

Qy      601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1882 AATTCTTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTG 1941

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Qy    641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
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Db   2002 TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAAT 2061

Qy    661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
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Db   2062 CAGATGATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCC 2121

Qy    681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2122 TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTT 2181

Qy    701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2182 GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAC 2241

Qy    721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 AGCCTAGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCC 2301

Qy    741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 ATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTG 2361

Qy    761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2362 ATCTTCACTGGGATCAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCT 2421

Qy    781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
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Db   2422 TATGCCTCCATCGATATTAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGAT 2481

Qy    801 ValGlnThrSerPhe 805
          |||||||||||||||
Db   2482 GTTCAGACCTCCTTT 2496
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RESULT 5
AAS21279

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ID   AAS21279 standard; cDNA; 3732 BP.
XX
AC   AAS21279;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human cDNA sequence encoding for PRO1885 polypeptide.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW   breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW   cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW   adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32678.
XX
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   09-DEC-1999;   99US-0170262.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31243.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   10-NOV-2000; 2000WO-US30873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   P-PSDB; AAU12207.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing
PT   PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT   lung, breast, prostate, cervical  -
XX
PS   Claim 3; Fig 71; 813pp; English.
XX
CC   AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful to detect other
CC   PRO polypeptides, to link bioactive molecules to cells expressing
CC   PRO polypeptides, to modulate biological activities of cells expressing
CC   PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample.
CC   Some of the 275 sequences are also useful to stimulate the release of
CC   tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC   proliferation or differentiation of chondrocytes, the proliferation or
CC   gene expression in pericyte cells, the release of proteoglycans from
CC   cartilage, the proliferation of inner ear utricular supporting cells or
CC   of T-lymphocytes, the release of a cytokine from peripheral blood
CC   monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC   the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC   skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC   to factor VIIA. The PRO polypeptides can be used in assays to identify
CC   molecules involved in binding interactions. The polynucleotides encoding
CC   PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy.
XX
SQ   Sequence 3732 BP; 1137 A; 722 C; 821 G; 1052 T; 0 other;

Alignment Scores:
Pred. No.:              0           Length:        3732
Score:                  4142.00     Matches:       802
Percent Similarity:     85.33%      Conservative:  1
Best Local Similarity:  85.23%      Mismatches:    2
Query Match:            96.53%      Indels:        138
DB:                     22          Gaps:          1

US-09-635-501-2 (1-805) x AAS21279 (1-3732)

Qy      1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     40 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 99
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```
Qy       21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      100 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 159

Qy       41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      160 TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA 219

Qy       61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      220 AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC 279

Qy       81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      280 CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTT 339

Qy      101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      340 CAGCAAAATGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTA 399

Qy      121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      400 AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA 459

Qy      141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      460 TGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAG 519

Qy      161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      520 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT 579

Qy      181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
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Db      580 GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGG 639

Qy      201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      640 GATTATTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC 699

Qy      221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      700 CAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT 759

Qy      241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      760 CATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGA 819

Qy      261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      820 TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCT 879

Qy      281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      880 TTGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG 939

Qy      301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
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Db      940 GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT 999

Qy      321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1000 CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG 1059

Qy      341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1060 AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG 1119

Qy      361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1120 TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAG 1179

Qy      381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1180 TATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC 1239

Qy      401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1240 CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCC 1299

Qy      421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1300 ATTGGTCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTC 1359

Qy      441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
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Db     1360 AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGG 1419

Qy      461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1420 TGGATGGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATG 1479

Qy      481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1480 AAGCGAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCC 1539

Qy      501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
            ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db     1540 GCATCTCTGTTCCATGTTTCTGATGATTACTCATTCATTCGATATTACACAAGGACCCTT 1599

Qy      521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
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Db     1600 TACCAATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCAC 1659

Qy      541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPhe--------------- 555
            |||||||||||||||||||||||||||||||||||||||
Db     1660 AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTT-GTAAGAAATACCTCA 1718

Qy      555 ------------------------------------------------------------ 555

Db     1719 AAATGTTGAACCTCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG 1778

Qy      555 ------------------------------------------------------------ 555

Db     1779 ATTTCTTTGTTCTAAAAAGAAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA 1838

Qy      555 ------------------------------------------------------------ 555

Db     1839 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGGCCACCTCTT 1898

Qy      555 ------------------------------------------------------------ 555

Db     1899 TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAAAGAGCGGTTTAG 1958

Qy      555 ------------------------------------------------------------ 555

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Qy      555 ------------------------------------------------------------ 555

Db     2019 GTCAAAGAGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCAA 2078

Qy      556 ------------------------------AsnMetLeuArgLeuGlyLysSerGluPro 565
                                          ||||||||||||||||||||||||||||||
Db     2079 AAGGCCCTGAACCCCCTTTTTTTGTGTAGCAATATGCTGAGGCTTGGAAAATCAGAACCC 2138

Qy      566 TrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeu 585
            |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
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Qy      586 AsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGly 605
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Db     2198 AACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGA 2257

Qy      606 TrpSerThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLeuLy 625
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
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Db    2258 TGGAGTACCGACTGGAGTCCATATGCAGACCCAAAGCATCAAAGTGAGGATAAGCCTAAA 2317

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Db    2318 ATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATC 2377

Qy     645 rSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPh 665
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Db    2378 ATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTT 2437

Qy     665 eGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheVa 685
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Db    2438 TGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGT 2497

Qy     685 lThrAlaProLysAsnValSerAspIleIleProArgThrGluValGluLysAlaIleAr 705
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Qy     705 gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe 725
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Qy     725 uGlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleVa 745
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Db    2618 GGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGT 2677

Qy     745 lPheGlyValValMetGlyValIleValValGlyIleValIleLeuIlePheThrGlyIl 765
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Qy     765 eArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnProTyrAlaSerIleAs 785
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Db    2738 CAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGA 2797

Qy     785 pIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAspValGlnThrSerPh 805
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Db    2798 TATTAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTT 2857

Qy     805 e 805
           |
Db    2858 T 2858

RESULT 6
AAS14880
ID   AAS14880 standard; cDNA; 2920 BP.
XX
AC   AAS14880;
XX
DT   20-DEC-2001  (first entry)
XX
DE   Human cDNA encoding novel human protein NHP #1.
XX
KW   Human; novel human protein; NHP; ss; antidiabetic; antirheumatic;
KW   antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
KW   neuroprotective; nootropic; antiparkinsonian;
KW   anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
KW   hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
KW   antimanic; immunosuppressive; cerebroprotective; antimicrobial;
KW   antiinflammatory; antibacterial; antipsoriatic; thyromimetic;
KW   immunomodulator; antiseborrheic; dermatological; vasoconstriction;
KW   gastrointestinal disorder; cardiovascular disorder; hypertension;
KW   coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
KW   cachexia; male infertility; impotence; testicular cancer; lung tumour;
KW   hyperproliferative disorder; pulmonary system disorder;
KW   central nervous system disorder; bone disorder;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   Huntington's disease; schizophrenia; mania; dementia; paranoia;
KW   panic disorder; learning disability; amyotropic lateral sclerosis;
KW   psychosis; autism; sleep disorder; immune system disorder;
KW   Hashimoto's thyroiditis; musculo-skeletal system disorders;
KW   multiple sclerosis; ischaemic brain injury; stroke; infectious disease;
KW   diabetes mellitus; immunological disorder; asthma; AIDS;
KW   acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
KW   inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
KW   neural system disorder; respiratory disorder; olfactory disorder;
KW   wound healing; chromosome X.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             213..2348
FT                   /*tag= a
FT                   /product= "NHP #1"
FT                   /transl_except= (pos:867..869,aa:Xaa)
FT                   /transl_except= (pos:930..932,aa:Xaa)
FT                   /transl_except= (pos:1707..1709,aa:Xaa)
FT                   /note= "Xaa= Any amino acid"
XX
PN   WO200174896-A1.
XX
PD   11-OCT-2001.
XX
PF   02-APR-2001; 2001WO-US10542.
XX
PR   03-APR-2000; 2000US-194118P.
PR   29-SEP-2000; 2000US-236384P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA,  Ni J,  Soppet DR,  Coleman TA,  Gentz RL,  Endress GA;
PI   Li Y,  Dillon PJ;
XX
DR   WPI; 2001-626394/72.
DR   P-PSDB; AAU09092.
XX
PT   New human proteins, useful for diagnosing, treating, preventing and/or
PT   prognosing disorders related to the proteins, including cardiovascular
PT   disorders, autoimmune disorders and reproductive disorders  -
XX
PS   Claim 1; Page 291-292; 318pp; English.
XX
CC   The invention relates to novel human proteins (NHP) and the
CC   nucleic acids that encode them and antibodies raised against them.
CC   The proteins, antibodies and nucleic acids are useful in the diagnosis,
CC   prognosis, prevention and/or treatment or diseases and/or disorders
CC   involving vasoconstriction, gastrointestinal disorders, cardiovascular
CC   disorders (e.g. hypertension, erectile dysfunction, high blood pressure,
CC   coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia,
CC   cachexia, disorders of small intestine, disorders of reproductive system
CC   (e.g. male infertility and/or impotence), testicular cancer, lung tumours
CC   and other hyperproliferative disorders, disorders of pulmonary system,
CC   central nervous system disorders, bone disorders, neurodegenerative
CC   diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's
CC   disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
CC   panic disorder, learning disabilities, amyotropic lateral sclerosis,
CC   psychoses, autism, sleep disorders), immune system disorders (e.g.
CC   Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
CC   central nervous system disorders (e.g. multiple sclerosis, ischaemic
CC   brain injury and/or stroke), infectious diseases, diabetes mellitus,
CC   immunological disorders (e.g. asthma, acquired immunodeficient syndrome
CC   (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
CC   sepsis, acne, psoriasis and lupus erythematosus), neural system
CC   disorders, respiratory disorders, olfactory disorders and wound
CC   healing. The present sequence encodes an NHP of the invention and
CC   is located on the X chromosome.
XX
SQ   Sequence 2920 BP; 897 A; 568 C; 654 G; 788 T; 13 other;

Alignment Scores:
Pred. No.:              0              Length:        2920
Score:                  4061.00        Matches:       763
Percent Similarity:     99.35%         Conservative:  1
Best Local Similarity:  99.22%         Mismatches:    4
Query Match:            94.64%         Indels:        1
DB:                     22             Gaps:          0
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US-09-635-501-2 (1-805) x AAS14880 (1-2920)

Qy          3 SerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThrIleGlu 22
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Db         35 AGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACCATTGAG 94

Qy         23 GluGlnAlaLysThrPheLeu-AspLysPheAsnHisGluAlaGluAspLeuPheTyrGl 42
              |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         95 GAACAGGCCAAGACATTTTTGGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCA 154

Qy         42 nSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGlnAsnMe 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 AAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACAT 214

Qy         62 tAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAlaGlnMe 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAAT 274

Qy         82 tTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeuGlnGl 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 GTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCA 334

Qy        102 nAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeuAsnTh 122
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Db        335 AAATGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATAC 394

Qy        122 rMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGluCysLe 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 AATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTT 454

Qy        142 uLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgLe 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 ATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCT 514

Qy        162 uTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluGl 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGA 574

Qy        182 uTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTy 202
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Db        575 GTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTA 634

Qy        202 rTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGlnLe 222
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Db        635 TTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTT 694

Qy        222 uIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeuHisAl 242
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Qy        242 aTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGlyCysLe 262
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Qy        262 uProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSerLeuTh 282
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Db        815 CCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATYTGTACWSTTTGAC 874

Qy        282 rValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGlnAlaTr 302
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db        875 AGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGRCCTG 934

Qy        302 pAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeuProAs 322
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Db        935 GGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAA 994

Qy        322 nMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGlnLysAl 342
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Qy        342 aValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMetCysTh 362
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Qy        362 rLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGlnTyrAs 382
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Db       1115 AAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGA 1174

Qy        382 pMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPheHisGl 402
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Db       1175 TATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGA 1234

Qy        402 uAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSerIleGl 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1235 AGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGG 1294

Qy        422 yLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeuLysGl 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1295 TCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACA 1354

Qy        442 nAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArgTrpMe 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1355 AGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGAT 1414

Qy        462 tValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMetLysAr 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1415 GGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCG 1474

Qy        482 gGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspProAlaSe 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1475 AGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATC 1534

Qy        502 rLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeuTyrGl 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1535 TCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTTTACCA 1594

Qy        522 nPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHisLysCy 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1595 ATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATG 1654

Qy        542 sAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeuGlyLy 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db       1655 TGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGNTTGGAAA 1714

Qy        562 sSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValAr 582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1715 ATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAG 1774

Qy        582 gProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSe 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1775 GCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTC 1834

Qy        602 rPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysValArgIl 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1835 TTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGAT 1894

Qy        622 eSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLe 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1895 AAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCT 1954

Qy        642 uPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMe 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1955 GTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGAT 2014

Qy        662 tIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAs 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2015 GATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAA 2074

Qy        682 nPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluValGluLy 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2075 TTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAA 2134

Qy        702 sAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLe 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||
Db       2135 GGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACGACAGCCT 2194
```

```
Qy     722 uGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTr 742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2195 AGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATG 2254

Qy     742 pLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeuIlePh 762
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2255 GCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTT 2314

Qy     762 eThrGlyIleArgAspArgLysLys 770
           |||||||||||||||||||||||||
Db    2315 CACTGGGATCAGAGATCGGAAGAAG 2339

RESULT 7
AAS14890
ID   AAS14890 standard; cDNA; 2911 BP.
XX
AC   AAS14890;
XX
DT   20-DEC-2001  (first entry)
XX
DE   Human cDNA encoding novel human protein NHP #11.
XX
KW   Human; novel human protein; NHP; ss; antidiabetic; antirheumatic;
KW   antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
KW   neuroprotective; nootropic; antiparkinsonian;
KW   anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
KW   hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
KW   antimanic; immunosuppressive; cerebroprotective; antimicrobial;
KW   antiinflammatory; antibacterial; antipsoriatic; thyromimetic;
KW   immunomodulator; antiseborrheic; dermatological; vasoconstriction;
KW   gastrointestinal disorder; cardiovascular disorder; hypertension;
KW   coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
KW   cachexia; male infertility; impotence; testicular cancer; lung tumour;
KW   hyperproliferative disorder; pulmonary system disorder;
KW   central nervous system disorder; bone disorder;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   Huntington's disease; schizophrenia; mania; dementia; paranoia;
KW   panic disorder; learning disability; amyotropic lateral sclerosis;
KW   psychosis; autism; sleep disorder; immune system disorder;
KW   Hashimoto's thyroiditis; musculo-skeletal system disorders;
KW   multiple sclerosis; ischaemic brain injury; stroke; infectious disease;
KW   diabetes mellitus; immunological disorder; asthma; AIDS;
KW   acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
KW   inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
KW   neural system disorder; respiratory disorder; olfactory disorder;
KW   wound healing.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             213..998
FT                   /*tag= a
FT                   /product= "NHP #11"
XX
PN   WO200174896-A1.
XX
PD   11-OCT-2001.
XX
PF   02-APR-2001; 2001WO-US10542.
XX
PR   03-APR-2000; 2000US-194118P.
PR   29-SEP-2000; 2000US-236384P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA,  Ni J,  Soppet DR,  Coleman TA,  Gentz RL,  Endress GA;
PI   Li Y,  Dillon PJ;
XX
DR   WPI; 2001-626394/72.
DR   P-PSDB; AAU09102.
XX
PT   New human proteins, useful for diagnosing, treating, preventing and/or
PT   prognosing disorders related to the proteins, including cardiovascular
PT   disorders, autoimmune disorders and reproductive disorders  -
XX
PS   Claim 1; Page 297-298; 318pp; English.
XX
CC   The invention relates to novel human proteins (NHP) and the
CC   nucleic acids that encode them and antibodies raised against them.
CC   The proteins, antibodies and nucleic acids are useful in the diagnosis,
CC   prognosis, prevention and/or treatment or diseases and/or disorders
CC   involving vasoconstriction, gastrointestinal disorders, cardiovascular
CC   disorders (e.g. hypertension, erectile dysfunction, high blood pressure,
CC   coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia,
CC   cachexia, disorders of small intestine, disorders of reproductive system
CC   (e.g. male infertility and/or impotence), testicular cancer, lung tumours
CC   and other hyperproliferative disorders, disorders of pulmonary system,
CC   central nervous system disorders, bone disorders, neurodegenerative
CC   diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's
CC   disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
CC   panic disorder, learning disabilities, amyotropic lateral sclerosis,
CC   psychoses, autism, sleep disorders), immune system disorders (e.g.
CC   Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
CC   central nervous system disorders (e.g. multiple sclerosis, ischaemic
CC   brain injury and/or stroke), infectious diseases, diabetes mellitus,
CC   immunological disorders (e.g. asthma, acquired immunodeficient syndrome
CC   (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
CC   sepsis, acne, psoriasis and lupus erythematosus), neural system
CC   disorders, respiratory disorders, olfactory disorders and wound
CC   healing. The present sequence encodes an NHP of the invention.
XX
SQ   Sequence 2911 BP; 896 A; 570 C; 655 G; 788 T; 2 other;

Alignment Scores:
Pred. No.:              0             Length:         2911
Score:                  4013.00       Matches:        763
Percent Similarity:     99.35%        Conservative:   1
Best Local Similarity:  99.22%        Mismatches:     4
Query Match:            93.52%        Indels:         3
DB:                     22            Gaps:           0

US-09-635-501-2 (1-805) x AAS14890 (1-2911)

Qy       3 SerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThrIleGlu 22
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35 AGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACCATTGAG 94

Qy      23 GluGlnAlaLysThrPheLeu-AspLysPheAsnHisGluAlaGluAspLeuPheTyrGl 42
           ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      95 GAACAGGCCAAGACATTTTTGGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCA 154

Qy      42 nSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGlnAsnMe 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     155 AAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACAT 214

Qy      62 tAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAlaGlnMe 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     215 GAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAAT 274

Qy      82 tTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeuGlnGl 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     275 GTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCA 334

Qy     102 nAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeuAsnTh 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     335 AAATGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATAC 394

Qy     122 rMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGluCysLe 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     395 AATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTT 454

Qy     142 uLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgLe 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     455 ATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCT 514

Qy     162 uTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluGl 182
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            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      515 CTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGA 574

Qy      182 uTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTy 202
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      575 GTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTA 634

Qy      202 rTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGlnLe 222
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      635 TTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTT 694

Qy      222 uIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeuHisAl 242
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      695 GATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGC 754

Qy      242 aTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGlyCysLe 262
            |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db      755 CTATGTGAGGCCAAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCT 814

Qy      262 uProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSerLeuTh 282
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      815 CCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGAC 874

Qy      282 rValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGlnAlaTr 302
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      875 AGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTG 934

Qy      302 pAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeuProAs 322
            ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db      935 GGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTT-GTATCTGTTGGTCTTCCTAA 993

Qy      322 nMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGlnLysAl 342
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 TATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAGAAAGC 1053

Qy      342 aValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMetCysTh 362
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054 AGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCAC 1113

Qy      362 rLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGlnTyrAs 382
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGA 1173

Qy      382 pMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPheHisGl 402
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 TATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGA 1233

Qy      402 uAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSerIleGl 422
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1234 AGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGG 1293

Qy      422 yLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeuLysGl 442
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1294 TCTTCTGTCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACA 1353

Qy      442 nAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArgTrpMe 462
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1354 AGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGAT 1413

Qy      462 tValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMetLysAr 482
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1414 GGTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCG 1473

Qy      482 gGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspProAlaSe 502
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1474 AGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATC 1533

Qy      502 rLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeuTyrGl 522
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1534 TCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTTTACCA 1593

Qy      522 nPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHisLysCy 542
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1594 ATTCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATG 1653

Qy      542 sAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeuGlyLy 562
            |||||||   |||||||||||||||||||||||||||||||||||||||||||   |||||
Db     1654 TGACATCTC-AACTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGNTTGGAAA 1712

Qy      562 sSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValAr 582
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1713 ATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAG 1772

Qy      582 gProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSe 602
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1773 GCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTC 1832

Qy      602 rPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysValArgIl 622
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1833 TTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGAT 1892

Qy      622 eSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLe 642
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1893 AAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCT 1952

Qy      642 uPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMe 662
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1953 GTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGAT 2012

Qy      662 tIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAs 682
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2013 GATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAA 2072

Qy      682 nPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluValGluLy 702
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2073 TTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAA 2132

Qy      702 sAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLe 722
            |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db     2133 GGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACGACAGCCT 2192

Qy      722 uGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTr 742
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2193 AGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATG 2252

Qy      742 pLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeuIlePh 762
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2253 GCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTT 2312

Qy      762 eThrGlyIleArgAspArgLysLys 770
            |||||||||||||||||||||||||
Db     2313 CACTGGGATCAGAGATCGGAAGAAG 2337
```

```
RESULT 8
AAZ59466
ID   AAZ59466 standard; DNA; 2262 BP.
XX
AC   AAZ59466;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human MPROT15 coding sequence #2.
XX
KW   MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;
KW   heart disease; apoplexy; heart disease; nervous denaturation; ds;
KW   Alzheimer's disease; hormone; cytokine.
XX
OS   Homo sapiens.
XX
PN   JP11318472-A.
XX
PD   24-NOV-1999.
XX
PF   22-JAN-1999;   99JP-0014949.
XX
PR   13-MAY-1998;   98GB-0010373.
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PR   18-AUG-1998;   98GB-0018009.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
DR   WPI; 2000-109268/10.
XX
PT   MPROT15 polypeptide and MPROT15 polynucleotides - useful for the
PT   treatment of hypertension, myocardial diseases, apoplexy, heart
PT   diseases, nervous denaturation, Alzheimer's disease etc.
XX
PS   Claim 18; Page 15; 22pp; Japanese.
XX
CC   This is coding sequence #2 of human MPROT15. The MPROT15 polynucleotide
CC   and polypeptide sequences can be used for the treatment of hypertension,
CC   myocardial diseases, apoplexy, heart diseases, nervous denaturation,
CC   Alzheimer's disease and diseases related to the processing of peptide
CC   hormones and cytokines.
XX
SQ   Sequence 2262 BP; 693 A; 450 C; 523 G; 596 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:        2262
Score:                  3740.50        Matches:       711
Percent Similarity:     90.57%         Conservative:  9
Best Local Similarity:  89.43%         Mismatches:    12
Query Match:            87.17%         Indels:        63
DB:                     21             Gaps:          3

US-09-635-501-2 (1-805) x AAZ59466 (1-2262)

Qy     11 LeuValAlaValThrAlaAlaGlnSerThrIleGluGluGlnAlaLysThrPheLeuAsp 30
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 CTTGTTGCTGTAACTGCTGCTCAGTCCACCATTGAGGAACAGGCCAAGACATTTTTGGAC 123

Qy     31 LysPheAsnHisGluAlaGluAspLeuPheTyrGlnSerSerLeuAlaSerTrpAsnTyr 50
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 AAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGCTTCTTGGAATTAT 183

Qy     51 AsnThrAsnIleThrGluGluAsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSer 70
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 AACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGGGGACAAATGGTCT 243

Qy     71 AlaPheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsn 90
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 GCCTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACAAGAAATTCAGAAT 303

Qy     91 LeuThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGlu 110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 CTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGCTCTCAGAA 363

Qy    111 AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly 130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 GACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCATCTACAGTACTGGA 423

Qy    131 LysValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGlu 150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACCAGGTTTGAATGAA 483

Qy    151 IleMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSer 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 ATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGAAAGCTGGAGATCT 543

Qy    171 GluValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMet 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 GAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTGAAAAATGAGATG 603

Qy    191 AlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsn 210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 GCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGACTATGAAGTAAAT 663

Qy    211 GlyValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPhe 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 GGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGTGGAACATACCTTT 723

Qy    231 GluGluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsn 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 GAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGCAAAGTTGATGAAT 783

Qy    251 AlaTyrProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMet 270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 GCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTTGCTTGGTGATATG 843

Qy    271 TrpGlyArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsn 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 TGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCCTTTGGACAGAAACCAAAC 903

Qy    291 IleAspValThrAspAlaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGlu 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 ATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAGAATATTCAAGGAG 963

Qy    311 AlaGluLysPhePheValSerValGlyLeuProAsnMetThrGlnGlyPheTrpGluAsn 330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGGATTCTGGGAAAAT 1023

Qy    331 SerMetLeuThrAspProGlyAsnValGlnLysAlaValCysHisProThrAlaTrpAsp 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 TCCATGCTAACGGACCCAGGAAATGTTCAGAAAGCAGTCTGCCATCCCACAGCTTGGGAC 1083

Qy    351 LeuGlyLysGlyAspPheArgIleLeuMetCysThrLysValThrMetAspAspPheLeu 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 CTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAATGGACGACTTCCTG 1143

Qy    371 ThrAlaHisHisGluMetGlyHisIleGlnTyrAspMetAlaTyrAlaAlaGlnProPhe 390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 ACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGCTGCACAACCTTTT 1203

Qy    391 LeuLeuArgAsnGlyAlaAsnGluGlyPheHisGluAlaValGlyGluIleMetSerLeu 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 CTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGAAATCATGTCACTT 1263

Qy    411 SerAlaAlaThrProLysHisLeuLysSerIleGlyLeuLeuSerProAspPheGlnGlu 430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 TCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCACCCGATTTTCAAGAA 1323

Qy    431 AspAsnGluThrGluIleAsnPheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeu 450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 GACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGATTGTTGGGACTCTG 1383

Qy    451 ProPheThrTyrMetLeuGluLysTrpArgTrpMetValPheLysGlyGluIleProLys 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGGGGAAATTCCCAAA 1443

Qy    471 AspGlnTrpMetLysLysTrpTrpGluMetLysArgGluIleValGlyValValGluPro 490
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Db   1444 GACCAGTGGATGAAAAAGTGGTGGGAGATGAAA--------------------------- 1476

Qy    491 ValProHisAspGluThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyr 510

Db   1476 ------------------------------------------------------------ 1476

Qy    511 SerPheIleArgTyrTyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeuCys 530
                     ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1477 ------------TATTACACAAGGACCCTTTACCAATTCCAGTTTCAAGAAGCACTTTGT 1524

Qy    531 GlnAlaAlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAla 550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1525 CAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAACTCTACAGAAGCT 1584

Qy    551 GlyGlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeu 570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1585 GGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCTGGACCCTAGCATTG 1644

Qy    571 GluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluPro 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1645 GAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAACTACTTTGAGCCC 1704
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Qy     591 LeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSerThrAspTrp 610
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1705 TTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATGGAGTACCGACTGG 1764

Qy     611 SerProTyrAlaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAsp 630
           ||||||:::
Db    1765 AGTCCATGG--------------------------------------------------- 1773

Qy     631 LysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerValAlaTyrAla 650
                                   |||:::::::::                :::
Db    1774 -----------------------GAAGTCTTCATTCTCTTGATTGTGTCCTCTGTGCCA 1809

Qy     651 MetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPheGlyGluGluAspVal 670
                 :::   |||:::               :::   |||:::   ||||||||||||
Db    1810 CAAGTGAAGATGTTTGTT---------------TTGTTTCTCTACAGGGAGGAGGATGTG 1854

Qy     671 ArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrAlaProLysAsn 690
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Db    1855 CGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAAT 1914

Qy     691 ValSerAspIleIleProArgThrGluValGluLysAlaIleArgMetSerArgSerArg 710
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1915 GTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGT 1974

Qy     711 IleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLeuGlyIleGlnProThr 730
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1975 ATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACA 2034

Qy     731 LeuGlyProProAsnGlnProProValSerIleTrpLeuIleValPheGlyValValMet 750
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2035 CTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATG 2094

Qy     751 GlyValIleValValGlyIleValIleLeuIlePheThrGlyIleArgAspArgLysLys 770
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2095 GGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAG 2154

Qy     771 LysAsnLysAlaArgSerGlyGluAsnProTyrAlaSerIleAspIleSerLysGlyGlu 790
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2155 AAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATATTAGCAAAGGAGAA 2214

Qy     791 AsnAsnProGlyPheGlnAsnThrAspAspValGlnThrSerPhe 805
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Db    2215 AATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTTT 2259
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RESULT 9
AAC84368
ID   AAC84368 standard; cDNA; 2638 BP.
XX
AC   AAC84368;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Mouse Zace2-5 protein encoding cDNA.
XX
KW   Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
KW   zinc metallopeptidase; blood pressure; zinc protease; hypertension;
KW   ventricular systolic dysfunction; renal impairment; heart failure;
KW   scleroderma renal crisis; atherosclerosis;. antiinflammatory; mouse;
KW   antiarthritic; bradykinin inactivator; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             106..2523
FT                   /*tag= a
FT                   /product= "Zace2-5"
FT                   /note= "the coding fragment is specifically claimed for"
XX
PN   WO200070032-A1.
XX
PD   23-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US11932.
XX
PR   13-MAY-1999;   99US-0311482.
PR   27-AUG-1999;   99US-0384706.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Piddington CS,  Petrie CR,  Shoemaker KE,  Bishop PD;
XX
DR   WPI; 2001-025018/03.
DR   P-PSDB; AAB48097.
XX
PT   Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
PT   bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
PT   associated with inflammation such as arthritis and enterocolitis -
XX
PS   Claim 10; Page 104-109; 125pp; English.
XX
CC   The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
CC   converting enzyme is a zinc metallopeptidase that plays roles in blood
CC   pressure regulation and fertility. Zace2 can be expressed by standard
CC   recombinant methodology. Zace2 polypeptides are useful for treating an
CC   inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
CC   diseases associated with inflammation like arthritis and enterocolitis,
CC   as targets for identifying modulators of zinc protease activity, for
CC   screening or identifying new angiotensin-converting enzyme (ACE)
CC   inhibitors, and as a basis for rational drug design for inhibitory
CC   molecules. The nucleic acids can be used to detect the expression of a
CC   Zace2 gene in a biological sample, as probes for in vivo diagnosis and
CC   for detecting and localizing Zace2 gene expression in tissue samples,
CC   to determine whether a subject's chromosomes contain a mutation in the
CC   Zace2 gene, and to detect aberrations associated with the Zace2 locus.
CC   Inhibitors of ACE are used for treating hypertension of various
CC   conditions, including left ventricular systolic dysfunction, progressive
CC   renal impairment, scleroderma renal crisis, congestive heart failure due
CC   to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
CC   used to treat infertility while Zace2 antagonists are used for inducing
CC   infertility. The present sequence represents a cDNA encoding the mouse
CC   Zace2-5 protein.
XX
SQ   Sequence 2638 BP; 802 A; 556 C; 611 G; 669 T; 0 other;

Alignment Scores:
Pred. No.:               0            Length:         2638
Score:                   3579.00      Matches:        661
Percent Similarity:      89.57%       Conservative:   60
Best Local Similarity:   82.11%       Mismatches:     84
Query Match:             83.41%       Indels:         0
DB:                      22           Gaps:           0

US-09-635-501-2 (1-805) x AAC84368 (1-2638)
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Qy       1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
           |||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db     106 ATGTCCAGCTCCTCCTGGCTCCTTCTCAGCCTTGTTGCTGTTACTACTGCTCAGTCCCTC 165

Qy      21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
              ||||||   ||||||||||||||||:::   ||||||   |||||||||||||||
Db     166 ACCGAGGAAAATGCCAAGACATTTTTAAACAACTTTAATCAGGAAGCTGAAGACCTGTCT 225

Qy      41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db     226 TATCAAAGTTCACTTGCTTCTTGGAATTATAATACTAACATTACTGAAGAAAATGCCCAA 285

Qy      61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
           |||:::   |||      |||||||||||||||   :::|||||||||      |||
Db     286 AAGATGAGTGAGGCTGCAGCCAAATGGTCTGCCTTTTATGAAGAACAGTCTAAGACTGCC 345

Qy      81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
           |||   :::   |||||||||||||||            :::|||   ||||||||||||||| |||
Db     346 CAAAGTTTCTCACTACAAGAAATCCAGACTCCGATCATCAAGCGTCAACTACAGGCCCTT 405

Qy     101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
           ||||||:::|||||||||   ||||||   ||||||:::|||:::|||||||||||||||
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Db     406 CAGCAAAGTGGGTCTTCAGCACTCTCAGCAGACAAGAACAAACAGTTGAACACAATTCTG 465

Qy     121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
           |||||||||||||||||||||||||||||||||||||||||||||||    |||||||||||
Db     466 AACACCATGAGCACCATTTACAGTACTGGAAAAGTTTGCAACCCAAAGAACCCACAAGAA 525

Qy     141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
           ||||||||||||||||||||||||:::||||||||||||    |||   |||||||||
Db     526 TGCTTATTACTTGAGCCAGGATTGGATGAAATAATGGCGACAAGCACAGACTACAACTCT 585

Qy     161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
           |||||||||||||||||    ||||||:::||||||||||||||||||||||||||||||
Db     586 AGGCTCTGGGCATGGGAGGGCTGGAGGGCTGAGGTTGGCAAGCAGCTGAGGCCGTTGTAT 645

Qy     181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
           ||||||||||||||||||||||||||||||||||||||||||||:::|||   |||||||||
Db     646 GAAGAGTATGTGGTACTGAAAAACGAGATGGCAAGAGCAAACAATTATAACGACTATGGG 705

Qy     201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
           ||||||||||||||||||||||      |||    |||||||||:::|||:::|||
Db     706 GATTATTGGAGAGGGGACTATGAAGCAGAGGGAGCAGATGGCTACAACTATAACCGTAAC 765

Qy     221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
           ||||||||||||||||||||    ||||||    ||||||||||||||||||||||||||
Db     766 CAGTTGATTGAAGATGTAGAACGTACCTTCGCAGAGATCAAGCCATTGTATGAGCATCTT 825

Qy     241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
           |||||||||||||||    ||||||||:::    ||||||||||||||||||||   |||
Db     826 CATGCCTATGTGAGGAGGAAGTTGATGGATACCTACCCTTCCTACATCAGCCCCACTGGA 885

Qy     261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     886 TGCCTCCCTGCCCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACCCT 945

Qy     281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
           |||||||||||||||    ||||||||||||||||||||||||||||||||:::::::|||
Db     946 TTGACTGTTCCCTTTGCACAGAAACCAAACATAGATGTTACTGATGCAATGATGAATCAG 1005

Qy     301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
           |||||||||:::|||||||||:::||||||||||||||||||||||||||||||||||||
Db    1006 GGCTGGGATGCAGAAAGGATATTTCAAGAGGCAGAGAAATTCTTTGTTTCTGTTGGCCTT 1065

Qy     321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
           |||:::||||||||||||||||||||    ||||||||||||||||:::|||   :::   :::
Db    1066 CCTCATATGACTCAAGGATTCTGGGCAAACTCTATGCTGACTGAGCCAGCAGATGGCCGG 1125

Qy     341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
           |||   |||||||||||||||||||||||||||||||||    |||||||||||||||   |||
Db    1126 AAAGTTGTCTGCCACCCCACAGCTTGGGATCTGGGACACGGAGACTTCAGAATCAAGATG 1185

Qy     361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
           ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db    1186 TGTACAAAGGTCACAATGGACAACTTCTTGACAGCCCATCACGAGATGGGACACATCCAA 1245

Qy     381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
           ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db    1246 TATGACATGGCATATGCCAGGCAACCTTTCCTGCTAAGAAACGGAGCCAATGAAGGGTTC 1305

Qy     401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1306 CATGAAGCTGTTGGAGAAATCATGTCACTTTCTGCAGCTACCCCCAAGCATCTGAAATCC 1365

Qy     421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
           ||||||||||||    ||||||||||||||||||:::||||||||||||||||||||||||
Db    1366 ATTGGTCTTCTGCCATCCGATTTTCAAGAAGATAGCGAAACAGAGATAAACTTCCTACTG 1425

Qy     441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1426 AAACAGGCATTGACAATTGTTGGAACACTACCGTTTACTTACATGTTAGAGAAGTGGAGG 1485

Qy     461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
           |||||||||||:::|||||||||||||||:::||||||||||||||||||||||||||||
Db    1486 TGGATGGTCTTTCGGGGTGAAATTCCCAAAGAGCAGTGGATGAAAAAGTGGTGGGAGATG 1545

Qy     481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
           |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db    1546 AAGCGGGAGATCGTTGGTGTGGTGGAGCCTCTGCCTCATGATGAAACATACTGTGACCCT 1605

Qy     501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db    1606 GCATCTCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAAGGACCATT 1665

Qy     521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
           ||||||||||||||||||||||||||||||||||||||||:::   |||   ||||||
Db    1666 TACCAATTCCAGTTTCAAGAAGCTCTTTGTCAAGCAGCTAAGTATAATGGTTCTCTGCAC 1725

Qy     541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
           ||||||||||||||||||||||||||||||||||||||||||      ||||||   |||
Db    1726 AAATGTGACATCTCAAATTCCACTGAAGCTGGGCAGAAGTTGCTCAAGATGCTGAGTCTT 1785

Qy     561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
           |||   |||||||||||||||    |||||||||||||||||||||:::||||||:::
Db    1786 GGAAATTCAGAGCCCTGGACCAAAGCCTTGGAAAATGTGGTAGGAGCAAGGAATATGGAT 1845

Qy     581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
           |||:::||||||||||||||||||||:::|||||||||    |||||||||:::||||||:::
Db    1846 GTAAAACCACTGCTCAATTACTTCCAACCGTTGTTTGACTGGCTGAAAGAGCAGAACAGA 1905

Qy     601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
           ||||||||||||||||||:::|||:::|||||||||||||||||||||||||||||||||
Db    1906 AATTCTTTTGTGGGGTGGAACACTGAATGGAGCCCATATGCCGACCAAAGCATTAAAGTG 1965

Qy     621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
           ||||||||||||||||||||||||||||      ||||||||||||      :::|||||||||
Db    1966 AGGATAAGCCTAAAATCAGCTCTTGGAGCTAATGCATATGAATGGACCAACAACGAAATG 2025

Qy     641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
           :::||||||||||||||||||||||||||||||||||:::||||||      :::||||||
Db    2026 TTCCTGTTCCGATCATCTGTTGCATATGCCATGAGAAAGTATTTTTCAATAATCAAAAAC 2085

Qy     661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
           |||   :::   |||   ||||||||||||||||||::::::|||||||||||||::::|||
Db    2086 CAGACAGTTCCTTTTCTAGAGGAAGATGTACGAGTGAGCGATTTGAAACCAAGAGTCTCC 2145

Qy     681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
           |||   ||||||||||||:::|||:::||||||||||||||||||||||||:::|||||||
Db    2146 TTCTACTTCTTTGTCACCTCACCCCAAAATGTGTCTGATGTCATTCCTAGAAGTGAAGTT 2205

Qy     701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
           |||   ||||||||||||||||||   ||||||||||||   |||   ||||||||||||
Db    2206 GAAGATGCCATCAGGATGTCTCGGGGCCGCATCAATGATGTCTTTGGCCTGAATGATAAC 2265

Qy     721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
           ||||||||||||||||||||   ||||||||||   ||||||   ||||||||||||:::
Db    2266 AGCCTGGAGTTTCTGGGGATTCACCCAACACTTGAGCCACCTTACCAGCCTCCTGTCACC 2325

Qy     741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
           ||||||||||||:::||||||||||||||||      ::::::|||||||||||:::||||||
Db    2326 ATATGGCTGATTATTTTTGGTGTTGTGATGGCACTGGTAGTGGTTGGCATCATCATCCTG 2385

Qy     761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
           |||   ||||||||||:::   ||||||||||||||||:::   :::      |||||||||
Db    2386 ATTGTCACTGGGATCAAAGGTCGAAAGAAGAAAAATGAAACAAAAAGAGAAGAGAACCCT 2445

Qy     781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
           |||   |||:::||||||   ||||||||:::|||   ||||||||||||:::||||||
Db    2446 TATGACTCGATGGACATTGGAAAAGGAGAAAGCAATGCAGGATTCCAAAACAGTGATGAT 2505

Qy     801 ValGlnThrSerPhe 805
              ||||||||||||
Db    2506 GCTCAGACTTCCTTT 2520

RESULT 10
AAC84370
ID   AAC84370 standard; cDNA; 2638 BP.
XX
```

```
AC   AAC84370;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Mouse Zace2-10 protein encoding cDNA.
XX
KW   Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
KW   zinc metallopeptidase; blood pressure; zinc protease; hypertension;
KW   ventricular systolic dysfunction; renal impairment; heart failure;
KW   scleroderma renal crisis; atherosclerosis;. antiinflammatory; mouse;
KW   antiarthritic; bradykinin inactivator; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             106..2523
FT                   /*tag= a
FT                   /product= "Zace2-10"
XX
PN   WO200070032-A1.
XX
PD   23-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US11932.
XX
PR   13-MAY-1999;   99US-0311482.
PR   27-AUG-1999;   99US-0384706.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Piddington CS,  Petrie CR,  Shoemaker KE,  Bishop PD;
XX
DR   WPI; 2001-025018/03.
DR   P-PSDB; AAB48098.
XX
PT   Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
PT   bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
PT   associated with inflammation such as arthritis and enterocolitis -
XX
PS   Disclosure; Page 113-118; 125pp; English.
XX
CC   The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
CC   converting enzyme is a zinc metallopeptidase that plays roles in blood
CC   pressure regulation and fertility. Zace2 can be expressed by standard
CC   recombinant methodology. Zace2 polypeptides are useful for treating an
CC   inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
CC   diseases associated with inflammation like arthritis and enterocolitis,
CC   as targets for identifying modulators of zinc protease activity, for
CC   screening or identifying new angiotensin-converting enzyme (ACE)
CC   inhibitors, and as a basis for rational drug design for inhibitory
CC   molecules. The nucleic acids can be used to detect the expression of a
CC   Zace2 gene in a biological sample, as probes for in vivo diagnosis and
CC   for detecting and localizing Zace2 gene expression in tissue samples,
CC   to determine whether a subject's chromosomes contain a mutation in the
CC   Zace2 gene, and to detect aberrations associated with the Zace2 locus.
CC   Inhibitors of ACE are used for treating hypertension of various
CC   conditions, including left ventricular systolic dysfunction, progressive
CC   renal impairment, scleroderma renal crisis, congestive heart failure due
CC   to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
CC   used to treat infertility while Zace2 antagonists are used for inducing
CC   infertility. The present sequence represents a cDNA encoding the mouse
CC   Zace2-10 protein.
XX
SQ   Sequence 2638 BP; 797 A; 557 C; 615 G; 669 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:         2638
Score:                  3561.00        Matches:        659
Percent Similarity:     89.32%         Conservative:   60
Best Local Similarity:  81.86%         Mismatches:     86
Query Match:            82.99%         Indels:         0
DB:                     22             Gaps:           0

US-09-635-501-2 (1-805) x AAC84370 (1-2638)

Qy      1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
Db    106 ATGTCCAGCTCCTCCTGGCTCCTTCTCAGCCTTGTTGCTGTTACTACTGCTCAGTCCCTC 165

Qy     21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
Db    166 ACCGAGGAAAATGCCAAGACATTTTTAAACAACTTTAATCAGGAGGCTGAAGACCTGTCT 225

Qy     41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
Db    226 TATCAAAGTTCACTTGCTTCTTGGAATTATAATACTAACATTACTGAAGAAAATGCCCAA 285

Qy     61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
Db    286 AAGATGAGTGAGGCTGCAGCCAAATGGTCTGCCTTTTATGAAGAACAGTCTAAGACTGCC 345

Qy     81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
Db    346 CAAAGTTTCTCACTACAAGAAATCCAGACTCCGATCATCAAGCGTCAACTACAGGCCCTT 405

Qy    101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
Db    406 CAGCAAAGTGGGTCTTCAGCACTCTCAGCAGACAAGAACAAACAGTTGAACACAATTCTG 465

Qy    121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
Db    466 AACACCATGAGCACCATTTACAGTACTGGAAAAGTTTGCAACCCAAGGAACCCACAAGAA 525

Qy    141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
Db    526 TGCTTATTACTTGAGCCAGGATTGGATGAAATAATGGCGACAAGCACAGACTACAACTCT 585

Qy    161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
Db    586 AGGCTCTGGGCATGGGAGGGCTGGAGGGCTGAGGTTGGCAAGCAGCTGAGGCCGTTGTAT 645

Qy    181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
Db    646 GAAGAGTATGTGGTCCTGAAAAACGAGATGGCAAGAGCAAACAATTATAACGACTATGGG 705

Qy    201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
Db    706 GATTATTGGAGAGGGGACTATGAAGCAGAGGGAGCAGATGGCTACAACTATAACCGTAAC 765

Qy    221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
Db    766 CAGTTGATTGAAGATGTAGAACGTACCTTCGCAGAGATCAAGCCATTGTATGAGCATCTT 825

Qy    241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
Db    826 CATGCCTATGTGAGGAGGAAGTTGATGGATACCTACCCTTCCTACATCAGCCCCACTGGA 885

Qy    261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
Db    886 TGCCTCCCTGCCCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACCCT 945

Qy    281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
Db    946 TTGACTGTTCCCTTTGCACAGAAACCAAACATAGATGTTACTGATGCAATGATGAATCAG 1005

Qy    301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
Db   1006 GGCTGGGATGCAGAAAGGATATTTCAAGAGGCAGAGAAATTCTTTGTTTCTGTTGGCCTT 1065

Qy    321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
Db   1066 CCTCATATGACTCAAGGATTCTGGGCAAACTCTATGCTGACTGAGCCAGCAGATGGCCGG 1125

Qy    341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
Db   1126 AAAGTTGTCTGCCACCCCACAGCTTGGGATCTGGGACACGGAGACTTCAGAATCAAGATG 1185
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Qy      361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
            ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db     1186 TGTACAAAGGTCACAATGGACAACTTCTTGACAGCCCATCACGAGATGGGACACATCCAA 1245

Qy      381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
            |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db     1246 TATGACATGGCATATGCCAGGCAACCTTTCCTGCTAAGAAACGGAGCCAATGAAGGGTTC 1305

Qy      401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1306 CATGAAGCTGTTGGAGAAATCATGTCACTTTCTGCAGCTACCCCCAAGCATCTGAAATCC 1365

Qy      421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
            ||||||||||||         |||||||||||||||:::|||||||||||||||||||||
Db     1366 ATTGGTCTTCTGCCATCCGATTTTCAAGAAGATAGCGAAACAGAGATAAACTTCCTACTG 1425

Qy      441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1426 AAACAGGCATTGACAATTGTTGGAACACTACCGTTTACTTACATGTTAGAGAAGTGGAGG 1485

Qy      461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
            ||||||||||:::|||||||||||||||||:::|||||||||||||||||||||||||||
Db     1486 TGGATGGTCTTTCGGGGTGAAATTCCCAAAGAGCAGTGGATGAAAAAGTGGTGGGAGATG 1545

Qy      481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
            |||||||||||||||||||||||||||||:::|||   ||||||||||||||||||||
Db     1546 AAGCGGGAGATCGTTGGTGTGGTGGAGCCTCTGCCTCGTGATGAAACATACTGTGACCCT 1605

Qy      501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db     1606 GCATCTCTGTTCCATGTTTCTAATGATTACTCATTCATTCGATATTACACAAGGACCATT 1665

Qy      521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
            ||||||||||||||||||||||||||||||||||||||||||:::   |||   ||||||
Db     1666 TACCAATTCCAGTTTCAAGAAGCTCTTTGTCAAGCAGCTAAGTATAATGGTTCTCTGCAC 1725

Qy      541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
            ||||||||||||||||||||||||||||||||||||||||||||     ||||||   |||
Db     1726 AAATGTGACATCTCAAATTCCACTGAAGCTGGGCAGAAGTTGCTCAAGATGCTGAGTCTT 1785

Qy      561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
            |||   |||||||||||||||   |||||||||||||||||||||||||:::||||||:::
Db     1786 GGAAATTCAGAGCCCTGGACCGAAGCCTTGGAAAATGTGGTAGGAGCAAGGAATATGGAT 1845

Qy      581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
            |||:::||||||||||||||||||:::|||||||||   ||||||||||:::|||||||:::
Db     1846 GTAAAACCACTGCTCAATTACTTCCAACCGTTGTTTGACTGGCTGAAAGAGCAGAACAGA 1905

Qy      601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
            |||||||||||||||||||:::|||:::||||||||||||||||||||||||||||||||
Db     1906 AATTCTTTTGTGGGGTGGAACACTGAATGGAGCCCATATGCCGACCAAAGCATTAAAGTG 1965

Qy      621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
            |||||||||||||||||||||||||      ||||||||||||    :::|||||||||
Db     1966 AGGATAAGCCTAAAATCAGCTCTTGGAGCTAATGCATATGAATGGACCAACAACGAAATG 2025

Qy      641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
            :::||||||||||||||||||||||||||||||||||||:::|||         :::||||||
Db     2026 TTCCTGTTCCGATCATCTGTTGCATATGCCATGAGAAAGTATTCTTCAATAATCAAAAAC 2085

Qy      661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
            |||   :::   |||   ||||||||||||||||||:::::::::||||||||||::|||
Db     2086 CAGACAGTTCCTTTTCTAGAGGAAGATGTACGAGTGAGTGATTTGAAACCAAGAGTCTCC 2145

Qy      681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
            |||   ||||||||||||:::||||:::|||||||||||||:::||||||||||:::||||||
Db     2146 TTCTACTTCTTTGTCACCTCACCCCAAAATGTGTCTGATGTCATTCCTAGAAGTGAAGTT 2205

Qy      701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
            |||   ||||||||||||||||||   ||||||||||||   |||   ||||||||||||
Db     2206 GAAGATGCCATCAGGATGTCTCGGGGCCGCATCAATGATGTCTTTGGCCTGAATGATAAC 2265

Qy      721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
            ||||||||||||||||||||||   ||||||||||   ||||||   |||||||||||||:::
Db     2266 AGCCTGGAGTTTCTGGGGATTCACCCAACACTTGAGCCACCTTACCAGCCTCCTGTCACC 2325

Qy      741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
            |||||||||||:::||||||||||||||||   ::::::|||||||||||||:::|||||||
Db     2326 ATATGGCTGATTATTTTGGTGTTGTGATGGCACTGGTAGTGGTTGGCATCATCATCCTG 2385

Qy      761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
            |||   ||||||||||:::   |||||||||||||||:::   :::      ||||||||||
Db     2386 ATTGTCACTGGGATCAAAGGTCGAAAGAAGAAAAATGAAACAAAAAGAGAAGAGAACCCT 2445

Qy      781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
            |||   |||:::||||||   |||||||||:::||||   ||||||||||||:::|||||||
Db     2446 TATGACTCGATGGACATTGGAAAAGGAGAAAGCAATGCAGGATTCCAAAACAGTGATGAT 2505

Qy      801 ValGlnThrSerPhe 805
               ||||||||||||
Db     2506 GCTCAGACTTCCTTT 2520
```

RESULT 11
AAC84367
ID   AAC84367 standard; DNA; 2415 BP.
XX
AC   AAC84367;
XX
DT   19-MAR-2001 (first entry)
XX
DE   Human Zace2 protein encoding degenerate sequence.
XX
KW   Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
KW   zinc metallopeptidase; blood pressure; zinc protease; hypertension;
KW   ventricular systolic dysfunction; renal impairment; heart failure;
KW   scleroderma renal crisis; atherosclerosis;. antiinflammatory; human;
KW   antiarthritic; bradykinin inactivator; ds.
XX
OS   Homo sapiens.
XX
PN   WO200070032-A1.
XX
PD   23-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US11932.
XX
PR   13-MAY-1999;   99US-0311482.
PR   27-AUG-1999;   99US-0384706.
XX
PA   (ZYMO) ZYMOGENETICS INC.
XX
PI   Piddington CS, Petrie CR, Shoemaker KE, Bishop PD;
XX
DR   WPI; 2001-025018/03.
DR   P-PSDB; AAB48095.
XX
PT   Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
PT   bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
PT   associated with inflammation such as arthritis and enterocolitis -
XX
PS   Disclosure; Page 103-104; 125pp; English.
XX
CC   The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
CC   converting enzyme is a zinc metallopeptidase that plays roles in blood
CC   pressure regulation and fertility. Zace2 can be expressed by standard
CC   recombinant methodology. Zace2 polypeptides are useful for treating an
CC   inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
CC   diseases associated with inflammation like arthritis and enterocolitis,
CC   as targets for identifying modulators of zinc protease activity, for
CC   screening or identifying new angiotensin-converting enzyme (ACE)
CC   inhibitors, and as a basis for rational drug design for inhibitory
CC   molecules. The nucleic acids can be used to detect the expression of a
CC   Zace2 gene in a biological sample, as probes for in vivo diagnosis and
CC   for detecting and localizing Zace2 gene expression in tissue samples,
CC   to determine whether a subject's chromosomes contain a mutation in the

```
CC   Zace2 gene, and to detect aberrations associated with the Zace2 locus.
CC   Inhibitors of ACE are used for treating hypertension of various
CC   conditions, including left ventricular systolic dysfunction, progressive
CC   renal impairment, scleroderma renal crisis, congestive heart failure due
CC   to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
CC   used to treat infertility while Zace2 antagonists are used for inducing
CC   infertility. The present sequence represents a degenerate sequence
CC   encoding the human Zace2 protein.
XX
SQ   Sequence 2415 BP; 494 A; 218 C; 398 G; 335 T; 970 other;

Alignment Scores:
Pred. No.:              0              Length:         2415
Score:                  3509.00        Matches:        644
Percent Similarity:     80.00%         Conservative:   0
Best Local Similarity:  80.00%         Mismatches:     161
Query Match:            81.78%         Indels:         0
DB:                     22             Gaps:           0

US-09-635-501-2 (1-805) x AAC84367 (1-2415)

Qy      1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
Db      1 ATGWSNWSNWSNWSNTGGYTNYTNYTNWSNYTNGTNGCNGTNACNGCNGCNCARWSNACN 60

Qy     21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
Db     61 ATHGARGARCARGCNAARACNTTYYTNGAYAARTTYAAYCAYGARGCNGARGAYYTNTTY 120

Qy     41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
Db    121 TAYCARWSNWSNYTNGCNWSNTGGAAYTAYAAYACNAAYATHACNGARGARAAYGTNCAR 180

Qy     61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
Db    181 AAYATGAAYAAYGCNGGNGAYAARTGGWSNGCNTTYYTNAARGARCARWSNACNYTNGCN 240

Qy     81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
Db    241 CARATGTAYCCNYTNCARGARATHCARAAYYTNACNGTNAARYTNCARYTNCARGCNYTN 300

Qy    101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
Db    301 CARCARAAYGGNWSNWSNGTNYTNWSNGARGAYAARWSNAARMGNYTNAAYACNATHYTN 360

Qy    121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
Db    361 AAYACNATGWSNACNATHTAYWSNACNGGNAARGTNTGYAAYCCNGAYAAYCCNCARGAR 420

Qy    141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
Db    421 TGYYTNYTNYTNGARCCNGGNYTNAAYGARATHATGGCNAAYWSNYTNGAYTAYAAYGAR 480

Qy    161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
Db    481 MGNYTNTGGGCNTGGGARWSNTGGMGNWSNGARGTNGGNAARCARYTNMGNCCNYTNTAY 540

Qy    181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
Db    541 GARGARTAYGTNGTNYTNAARAAYGARATGGCNMGNGCNAAYCAYTAYGARGAYTAYGGN 600

Qy    201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
Db    601 GAYTAYTGGMGNGGNGAYTAYGARGTNAAYGGNGTNGAYGGNTAYGAYTAYWSNMGNGGN 660

Qy    221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
Db    661 CARYTNATHGARGAYGTNGARCAYACNTTYGARGARATHAARCCNYTNTAYGARCAYYTN 720

Qy    241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
Db    721 CAYGCNTAYGTNMGNGCNAARYTNATGAAYGCNTAYCCNWSNTAYATHWSNCCNATHGGN 780

Qy    261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
Db    781 TGYYTNCCNGCNCAYYTNYTNGGNGAYATGTGGGGNMGNTTYTGGACNAAYYTNTAYWSN 840

Qy    281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
Db    841 YTNACNGTNCCNTTYGGNCARAARCCNAAYATHGAYGTNACNGAYGCNATGGTNGAYCAR 900

Qy    301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
Db    901 GCNTGGGAYGCNCARMGNATHTTYAARGARGCNGARAARTTYTTYGTNWSNGTNGGNYTN 960

Qy    321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
Db    961 CCNAAYATGACNCARGGNTTYTGGGARAAYWSNATGYTNACNGAYCCNGGNAAYGTNCAR 1020

Qy    341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
Db   1021 AARGCNGTNTGYCAYCCNACNGCNTGGGAYYTNGGNAARGGNGAYTTYMGNATHYTNATG 1080

Qy    361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
Db   1081 TGYACNAARGTNACNATGGAYGAYTTYYTNACNGCNCAYCAYGARATGGGNCAYATHCAR 1140

Qy    381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
Db   1141 TAYGAYATGGCNTAYGCNGCNCARCCNTTYYTNYTNMGNAAYGGNGCNAAYGARGGNTTY 1200

Qy    401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
Db   1201 CAYGARGCNGTNGGNGARATHATGWSNYTNWSNGCNGCNACNCCNAARCAYYTNAARWSN 1260

Qy    421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
Db   1261 ATHGGNYTNYTNWSNCCNGAYTTYCARGARGAYAAYGARACNGARATHAAYTTYYTNYTN 1320

Qy    441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
Db   1321 AARCARGCNYTNACNATHGTNGGNACNYTNCCNTTYACNTAYATGYTNGARAARTGGMGN 1380

Qy    461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
Db   1381 TGGATGGTNTTYAARGGNGARATHCCNAARGAYCARTGGATGAARAARTGGTGGGARATG 1440

Qy    481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
Db   1441 AARMGNGARATHGTNGGNGTNGTNGARCCNGTNCCNCAYGAYGARACNTAYTGYGAYCCN 1500

Qy    501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
Db   1501 GCNWSNYTNTTYCAYGTNWSNAAYGAYTAYWSNTTYATHMGNTAYTAYACNMGNACNYTN 1560

Qy    521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
Db   1561 TAYCARTTYCARTTYCARGARGCNYTNTGYCARGCNGCNAARCAYGARGGNCCNYTNCAY 1620

Qy    541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
Db   1621 AARTGYGAYATHWSNAAYWSNACNGARGCNGGNCARAARYTNTTYAAYATGYTNMGNYTN 1680

Qy    561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
Db   1681 GGNAARWSNGARCCNTGGACNYTNGCNYTNGARAAYGTNGTNGGNGCNAARAAYATGAAY 1740

Qy    581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
Db   1741 GTNMGNCCNYTNYTNAAYTAYTTYGARCCNYTNTTYACNTGGYTNAARGAYCARAAYAAR 1800

Qy    601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
Db   1801 AAYWSNTTYGTNGGNTGGWSNACNGAYTGGWSNCCNTAYGCNGAYCARWSNATHAARGTN 1860

Qy    621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
```

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                 |||      |||   |||   ||||||||||||||||||||||||||||||||||||
Db   1861 MGNATHWSNYTNAARWSNGCNYTNGGNGAYAARGCNTAYGARTGGAAYGAYAAYGARATG 1920

Qy    641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
          |||  |||          |||||||||||||||  |||||||||   |||||||||||
Db   1921 TAYYTNTTYMGNWSNWSNGTNGCNTAYGCNATGMGNCARTAYTTYYTNAARGTNAARAAY 1980

Qy    661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
          |||||||||  ||||||||||||||||||  |||||||||  ||||||    |||
Db   1981 CARATGATHYTNTTYGGNGARGARGAYGTNMGNGTNGCNAAYYTNAARCCNMGNATHWSN 2040

Qy    681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
          ||||||||||||||||||||||||||||||||||   ||||||||||||   |||||||||
Db   2041 TTYAAYTTYTTYGTNACNGCNCCNAARAAYGTNWSNGAYATHATHCCNMGNACNGARGTN 2100

Qy    701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
          ||||||||||||   |||            |||||||||||||||      |||||||||
Db   2101 GARAARGCNATHMGNATGWSNMGNWSNMGNATHAAYGAYGCNTTYMGNYTNAAYGAYAAY 2160

Qy    721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
                ||||||  ||||||||||||||   ||||||||||||||||||||||||
Db   2161 WSNYTNGARTTYYTNGGNATHCARCCNACNYTNGGNCCNCCNAAYCARCCNCCNGTNWSN 2220

Qy    741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 ATHTGGYTNATHGTNTTYGGNGTNGTNATGGGNGTNATHGTNGTNGGNATHGTNATHYTN 2280

Qy    761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
          ||||||||||||||   |||   ||||||||||||||||||      ||||||||||||
Db   2281 ATHTTYACNGGNATHMGNGAYMGNAARAARAARAAYAARGCNMGNWSNGGNGARAAYCCN 2340

Qy    781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
          ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db   2341 TAYGCNWSNATHGAYATHWSNAARGGNGARAAYAAYCCNGGNTTYCARAAYACNGAYGAY 2400

Qy    801 ValGlnThrSerPhe 805
          |||||||||   |||
Db   2401 GTNCARACNWSNTTY 2415
```

RESULT 12
AAS42515
ID   AAS42515 standard; cDNA; 3474 BP.
XX
AC   AAS42515;
XX
DT   18-DEC-2001 (first entry)
XX
DE   Human cDNA encoding an mddt protein, clone LI:347572.1:2000MAY01.
XX
KW   Human; molecules for disease detection and treatment; mddt; ss;
KW   Antiarteriosclerotic; hepatotropic; antipsoriatic; cytostatic;
KW   immunosuppressive; antidiabetic; antiasthmatic; neuroprotective;
KW   osteopathic; antiarthritic; cell proliferative disorder;
KW   arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma;
KW   leukaemia; breast cancer; autoimmune disorder; AIDS;
KW   acquired immunodeficiency syndrome; Addison's disease;
KW   diabetes mellitus; asthma; multiple sclerosis; osteoarthritis.
XX
OS   Homo sapiens.
XX
PN   WO200162922-A2.
XX
PD   30-AUG-2001.
XX
PF   21-FEB-2001; 2001WO-US05896.
XX
PR   24-FEB-2000; 2000US-0185213.
PR   16-MAY-2000; 2000US-0205232.
PR   17-MAY-2000; 2000US-0205285.
PR   17-MAY-2000; 2000US-0205286.
PR   17-MAY-2000; 2000US-0205287.
PR   17-MAY-2000; 2000US-0205323.
PR   17-MAY-2000; 2000US-0205324.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;
PI   Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE;
PI   Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL;
PI   Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A;
PI   Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W;
PI   Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
XX
DR   WPI; 2001-570631/64.
DR   P-PSDB; AAU25463.
XX
PT   New disease detection and treatment molecule polynucleotides and
PT   polypeptides, useful for diagnosis and treatment of arteriosclerosis,
PT   cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus,
PT   asthma and multiple sclerosis -
XX
PS   Claim 1; Page 139-140; 183pp; English.
XX
CC   The invention relates to novel human molecules for disease
CC   detection and treatment (mddt proteins) and the polynucleotides encoding
CC   them. The MDDT polynucleotides and polypeptides are useful for diagnostic
CC   and therapeutic purposes e.g. to diagnose and treat cell proliferative
CC   disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g.
CC   adenocarcinoma, leukaemia and breast cancer) autoimmune disorders
CC   (e.g. acquired immunodeficiency syndrome (AIDS) and Addison's disease)
CC   diabetes mellitus, asthma, multiple sclerosis, osteoarthritis, and many
CC   more diseases given in the specification. The present sequence
CC   encodes an mddt protein of the invention.
XX
SQ   Sequence 3474 BP; 1019 A; 696 C; 781 G; 978 T; 0 other;

```
Alignment Scores:
Pred. No.:              6.19e-294    Length:         3474
Score:                  3119.00      Matches:        730
Percent Similarity:     85.94%       Conservative:   22
Best Local Similarity:  83.43%       Mismatches:     51
Query Match:            72.69%       Indels:         72
DB:                     22           Gaps:           10
```

US-09-635-501-2 (1-805) x AAS42515 (1-3474)

```
Qy      1 MetSerSerSer-SerTrpLeuLeuLeuSerLeuValAla-ValThr-AlaAlaGlnSer 19
          |||||||||||| ||||||||||||||||||||||||||| |||||| ||||||||||||
Db     39 ATGTCAAGCTCCTTCCTGGCTCCTTCTCAGCCTTGTTGCCTGTAACTGGCTGCTCAGTCC 98

Qy     20 ThrIleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeu 39
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     99 ACCATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTG 158

Qy     40 PheTyrGlnSerSer-LeuAlaSer-TrpAsnTyrAsnThrAsnIleThrGluGluAsnV 59
          ||||||||||||||| :::|||||| ||||||||||||||||||||||||||||||||||
Db    159 TTCTATCAAAGTTCACGTTGCTTCCTTGGAATTATAACACCAATATTACTGAAGAGAATG 218

Qy     59 alGln-AsnMetAsn---AsnAlaGlyAspLys------TrpSerAlaPheLeuLysGlu 75
          ||||| ||||||      ||||||:::              |||    |||    ||||||
Db    219 TCCAACAACATGCAATAAGTTGCTGGCGAGACAAATGTGTCTAGCCCTTTTTACAAGGAA 278

Qy     76 GlnSerThrLeuAlaGln-MetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLe 95
          |||||||||||||||||| ||||||||||||||            |||    |||
Db    279 CAGTCCACACTTGCCCAAGATGTATCCACTACAA------GCAAACTTCACGACATCTCC 332

Qy     95 uGlnLeuGlnAlaLeuGlnGlnAsnGly-----------------------SerSerVa 107
             :::   |||        :::|||                          ||||||
Db    333 ACATGTCAACGCTTCAGCTGTGCACGGCTTCTTCAAGCCATAAAACTGTGAGTCTTCAGG 392

Qy    107 lLeuSer------GluAspLysSerLys-ArgLeuAsnThrIleLeuAsnThrMet---- 123
              |||           :::||||||  |||||||||||||||      |||
Db    393 TTGGTCATCACGAAGCACAGAGAGCAAACCGGTTGAACACAATTTCTAATATACAAATGG 452

Qy    124 -----SerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGluCysL 142
                 :::        |||||||||         ||||||||||||||||||||||||
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Db    453 AGCCACCAATCCTAACAGTAACTGGAAAACGTCGTAACCCAGATAATCCACAAGAATGCT 512

Qy    142 euLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgL 162
Db    513 TATTACTTGAACCAGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGC 572

Qy    162 euTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluG 182
Db    573 TCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAG 632

Qy    182 luTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAsp-Tyr-GlyAs 201
Db    633 AGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTTATTGGGGA 692

Qy    201 pTyrTrpArgGlyAspTyrGluValAsnGlyValAsp---GlyTyrAspTyrSerArgGl 220
Db    693 TTATTGGAGAGGAGACTATGAAGTAAATGGGGTAAATAGTGGATATGATTACAGCCGCGG 752

Qy    220 yGlnLeuIleGluAspValGluHisThr-PheGluGluIleLysProLeuTyr-GluHis 239
Db    753 CCAGTTGATTGAAGATGTGGAACATACCTGTTGAAGAGATTAAACCATTGATAGGAACAT 812

Qy    240 LeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIle 259
Db    813 CTTCAGCCCTATGTGAGGGCCAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATT 872

Qy    260 GlyCysLeuProAlaHisLeuLeuGlyAspMetTrp-GlyArgPheTrpThrAsnLeuTy 279
Db    873 GGATGCCTCCCTGCTCATTTGCTTGGTGATATGTGCGGGTAGATTTTGGACAAATCTGTA 932

Qy    279 rSerLeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAs 299
Db    933 CTCTTTGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGA 992

Qy    299 pGlnAlaTrpAspAlaGlnArgIlePheLysGluAla-GluLysPhePheValSerValG 319
Db    993 CCAGGCCTGGGATGCACAGAGAATATTCAAGGAGTCCGCAGAACTTCTTTGTATCTGTTG 1052

Qy    319 lyLeuProAsnMetThrGlnGlyPheTrp-GluAsnSerMetLeu-ThrAspProGlyAs 338
Db   1053 GTCTTCCTTATATGACTCTAGGATTCTGCGGCAAATTCCATGCTATACGGACCCAGGAAA 1112

Qy    338 nValGlnLysAlaValCysHis-ProThrAlaTrpAspLeuGlyLysGlyAspPheArg- 357
Db   1113 TGTTCAGAAAGCACTCTGCCATCCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGAG 1172

Qy    358 IleLeuMetCysThrLys-ValThrMetAspAspPheLeuThrAlaHisHisGluMetGl 377
Db   1173 ATCCTTATGTGCACAAAGGGTAACAATGGACGACTTCCTGACAGCTCATCATGAGATGGG 1232

Qy    377 yHisIleGlnTyrAspMetAlaTyrAlaAlaGlnPro-PheLeuLeuArg-AsnGlyAla 396
Db   1233 GCATATCCAGTATGATATGGCATATGCCGGCCAACCTTTTTCTGCTAAGGAAATGGAGCT 1292

Qy    397 -AsnGluGlyPheHisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLy 416
Db   1293 TAATGAAGGATTCCATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAA 1352

Qy    416 sHisLeuLysSerIleGlyLeuLeuSerProAspPheGln---GluAspAsnGluThrGl 435
Db   1353 GCATTTAAAATCCATTGGTCTTCTGTCACCCGAGTTTTCAACGAACGACAATGAAACAGA 1412

Qy    435 uIleAsnPheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMe 455
Db   1413 AATAAACTTCCTGCTCAAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTACAT 1472

Qy    455 tLeuGluLysTrpArgTrpMetValPheLys-GlyGluIleProLysAspGlnTrpMetL 475
Db   1473 GTTAGAGAAGTGGAGGTGGATGGTCTTTAAACGGGGAAATTCCCAAAGACCAGTGGGTGA 1532

Qy    475 ysLys-TrpTrpGluMetLysArgGlu-IleValGlyVal-ValGluProValProHisA 494
Db   1533 AAAAGGTGGTGGGAGATGAAGCGAAAGAATAGTTGGGGTGTGTGGAACCTGTGCCCCATG 1592

Qy    494 spGluThrTyr-CysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIle 513
Db   1593 ATGAAACATATCTGTGACCCCGCATCTCTGTTCCATGTTTCTAATGATTACTCATTCATT 1652

Qy    514 ArgTyrTyrThrArgThrLeu-TyrGlnPheGlnPheGln-GluAlaLeu-CysGlnAla 532
Db   1653 CGATATTACACAAGGACCCTGTTACCAATTCCAGTTTCAAAGAAGCACTTTTGTCAAGCA 1712

Qy    533 AlaLysHisGluGlyProLeuHisLys-CysAspIle-SerAsnSerThrGlu---AlaG 551
Db   1713 GCTAAACATGAAGGCCCTCTGCACAAATTGTGACATTCTCAAATTCTACAGAACGTCGTG 1772

Qy    551 lyGlnLys-LeuPheAsnMetLeuArgLeuGlyLys-SerGluProTrpThrLeuAlaLe 570
Db   1773 GACAGAACACTGTTCAATATGCTGAGGCTTGGAAAACTCAGAACCCTGGACCCTAGCATT 1832

Qy    570 uGluAsnValVal-GlyAlaLysAsnMetAsnValArgPro-LeuLeuAsnTyrPheGlu 589
Db   1833 GGAAAATGTTGTAAGGACCAAAGAACATGAATGTAAGGCCACCTGCTCAACTACTTTGAG 1892

Qy    590 ProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSerThrAsp 609
Db   1893 CCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATGGAGTACCGAC 1952

Qy    610 TrpSerProTyrAlaAspGlnSerIle-LysValArgIleSerLeuLysSerAlaLeuGl 629
Db   1953 TGGAGTCCATATGCAGACCACAGCATCACAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 2012

Qy    629 y-AspLysAlaTyrGluTrpAsnAsp-AsnGluMetTyrLeuPheArgSerSer-ValAl 648
Db   2013 CAGATAAAGCATATGAATGGAACGACCAATGAAATGTACCTGTTCCGATCATCTGGTTGG 2072

Qy    648 aTyrAla---MetArgGlnTyrPheLeu-LysValLysAsnGlnMetIleLeuPheGlyG 667
Db   2073 ATATTGTTAATTGAGGCAGTACTTTTTAACAAGTAAAAAATCAGATGATTCTTTTGGGG 2132

Qy    667 luGluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrA 687
Db   2133 AGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTG 2192

Qy    687 laProLysAsnValSer-AspIleIleProArg-ThrGluValGluLysAlaIleArgMe 706
Db   2193 CACCTAAAAATGTGTCTGGATATCATTCCTAGAAACTGAAGTTGAAAAGGCCATCAGGAT 2252

Qy    706 tSerArgSerArg-IleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLeuG 726
Db   2253 GTCCCGGAGCCGTACTCCATGATGCTTTCCGTCTGAATGACGACAGCCTAGAGTTTCTGG 2312

Qy    726 lyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleValP 746
Db   2313 GGATACACCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTT 2372

Qy    746 heGlyValValMetGlyValIleValValGly-IleValIleLeu-IlePheThrGlyIl 765
Db   2373 TTGGAGTTGTGATGGGAGTGATAATTGTTGGCCATGGTCATCCTGGATCTTCACTGGAAT 2432

Qy    765 eArgAspArgLysLysLysAsnLysAlaArgSerGlyGlu-AsnPro-TyrAlaSerIle 784
Db   2433 CAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAATAATCCTTTATGCCTCCATC 2492

Qy    785 AspIleSerLysGlyGlu--AsnAsnProGlyPheGlnAsnThrAspAspValGlnThrS 804
Db   2493 GATATTAGCTAAGGAGTATAAATAATCCAGGATTCCGAAACACTGATGATGTTCAGACCT 2552

Qy    804 erPhe 805
Db   2553 CCTTT 2557

RESULT 13
AAC84369
ID   AAC84369 standard; DNA; 2415 BP.
XX
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```
AC   AAC84369;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Mouse Zace2-5 protein encoding degenerate sequence.
XX
KW   Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
KW   zinc metallopeptidase; blood pressure; zinc protease; hypertension;
KW   ventricular systolic dysfunction; renal impairment; heart failure;
KW   scleroderma renal crisis; atherosclerosis;. antiinflammatory; mouse;
KW   antiarthritic; bradykinin inactivator; ds.
XX
OS   Mus sp.
XX
PN   WO200070032-A1.
XX
PD   23-NOV-2000.
XX
PF   03-MAY-2000; 2000WO-US11932.
XX
PR   13-MAY-1999;   99US-0311482.
PR   27-AUG-1999;   99US-0384706.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Piddington CS,  Petrie CR,  Shoemaker KE,  Bishop PD;
XX
DR   WPI; 2001-025018/03.
DR   P-PSDB; AAB48097.
XX
PT   Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
PT   bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
PT   associated with inflammation such as arthritis and enterocolitis -
XX
PS   Disclosure; Page 112-113; 125pp; English.
XX
CC   The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
CC   converting enzyme is a zinc metallopeptidase that plays roles in blood
CC   pressure regulation and fertility. Zace2 can be expressed by standard
CC   recombinant methodology. Zace2 polypeptides are useful for treating an
CC   inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
CC   diseases associated with inflammation like arthritis and enterocolitis,
CC   as targets for identifying modulators of zinc protease activity, for
CC   screening or identifying new angiotensin-converting enzyme (ACE)
CC   inhibitors, and as a basis for rational drug design for inhibitory
CC   molecules. The nucleic acids can be used to detect the expression of a
CC   Zace2 gene in a biological sample, as probes for in vivo diagnosis and
CC   for detecting and localizing Zace2 gene expression in tissue samples,
CC   to determine whether a subject's chromosomes contain a mutation in the
CC   Zace2 gene, and to detect aberrations associated with the Zace2 locus.
CC   Inhibitors of ACE are used for treating hypertension of various
CC   conditions, including left ventricular systolic dysfunction, progressive
CC   renal impairment, scleroderma renal crisis, congestive heart failure due
CC   to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
CC   used to treat infertility while Zace2 antagonists are used for inducing
CC   infertility. The present sequence represents a degenerate sequence
CC   encoding the mouse Zace2-5 protein.
XX
SQ   Sequence 2415 BP; 488 A; 228 C; 397 G; 324 T; 978 other;

Alignment Scores:
Pred. No.:              1.08e-272      Length:         2415
Score:                  2899.00        Matches:        526
Percent Similarity:     71.06%         Conservative:   46
Best Local Similarity:  65.34%         Mismatches:     233
Query Match:            67.56%         Indels:         0
DB:                     22             Gaps:           0

US-09-635-501-2 (1-805) x AAC84369 (1-2415)

Qy        1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
              |||         |||             |||||||||||  ||||||
Db        1 ATGWSNWSNWSNWSNTGGYTNYTNYTNWSNYTNGTNGCNGTNACNACNGCNCARWSNYTN 60

Qy       21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
              ||||||  |||||||||||    :::  ||||||  |||||||||||
Db       61 ACNGARGARAAYGCNAARACNTTYYTNAAYAAYTTYAAYCARGARGCNGARGAYYTNWSN 120

Qy       41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
            |||||          |||  ||||||||||||||||||||||||||||||  |||
Db      121 TAYCARWSNWSNYTNGCNWSNTGGAAYTAYAAYACNAAYATHACNGARGARAAYGCNCAR 180

Qy       61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
               |||     |||     ||||||  ||||||   :::||||||         |||
Db      181 AARATGWSNGARGCNGCNGCNAARTGGWSNGCNTTYTAYGARGARCARWSNAARACNGCN 240

Qy       81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100
            |||   :::        ||||||||||||        :::|||   |||  ||||||
Db      241 CARWSNTTYWSNYTNCARGARATHCARACNCCNATHATHAARMGNCARYTNCARGCNYTN 300

Qy      101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
            ||||||  |||                 |||||:::|||:::  |||||||||
Db      301 CARCARWSNGGNWSNWSNWSNGCNYTNWSNGCNGAYAARAAYAARCARYTNAAYACNATHYTN 360

Qy      121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
            |||||||||   |||   |||  ||||||||||||||||||||||   ||||||||||||
Db      361 AAYACNATGWSNACNATNTAYWSNACNGGNAARGTNTGYAAYCCNAARAAYCCNCARGAR 420

Qy      141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
            |||         |||||||||   :::||||||||||||             |||||||||
Db      421 TGYYTNYTNYTNGARCCNGGNYTNGAYGARATHATGGCNACNWSNACNGAYTAYAAYWSN 480

Qy      161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
                  ||||||||||||   |||   :::||||||||||||||||      |||   |||
Db      481 MGNYTNTGGGCNTGGGARGGNTGGMGNGCNGARGTNGGNAARCARYTNMGNCCNYTNTAY 540

Qy      181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200
            |||||||||||||||   |||||||||||||||   ||||||:::|||   |||||||||
Db      541 GARGARTAYGTNGTNYTNAARAAYGARATGGCNMGNGCNAAYAAYTAYAAYGAYTAYGGN 600

Qy      201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
            |||||||||   ||||||||||||       |||   |||||||||:::|||:::
Db      601 GAYTAYTGGMGNGGNGAYTAYGARGCNGARGGNGCNGAYGGNTAYAAYTAYAAYMGNAAY 660

Qy      221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
            |||   |||||||||||||||     ||||||   ||||||||||||   |||||||||
Db      661 CARYTNATHGARGAYGTNGARMGNACNTTYGCNGARATHAARCCNYTNTAYGARCAYYTN 720

Qy      241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260
            ||||||||||||      |||   |||:::   ||||||   ||||||   |||   |||
Db      721 CAYGCNTAYGTNMGNMGNAARYTNATGGAYACNTAYCCNWSNTAYATHWSNCCNACNGGN 780

Qy      261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 280
            |||   |||||||||         |||||||||||||||   ||||||||||||   |||
Db      781 TGYYTNCCNGCNCAYYTNYTNGGNGAYATGTGGGGNMGNTTYTGGACNAAYYTNTAYCCN 840

Qy      281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
               ||||||||||||   ||||||||||||||||||||||||||||||||||:::::|||
Db      841 YTNACNGTNCCNTTYGCNCARAARCCNAAYATHGAYGTNACNGAYGCNATGATGAAYCAR 900

Qy      301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 320
               |||||||||:::   ||||||:::||||||||||||||||||||||   ||||||
Db      901 GGNTGGGAYGCNGARMGNATHTTYCARGARGCNGARAARTTYTTYGTNWSNGTNGGNYTN 960

Qy      321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
            |||:::||||||||||||||||||   |||   |||   |||:::|||   :::
Db      961 CCNCAYATGACNCARGGNTTYTGGGCNAAYWSNATGYTNACNGARCCNGCNGAYGGNMGN 1020

Qy      341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360
            |||   ||||||||||||||||||||||||   |||   |||||||||   |||   |||
Db     1021 AARGTNGTNTGYCAYCCNACNGCNTGGGAYYTNGGNCAYGGNGAYTTYMGNATHAARATG 1080

Qy      361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
            |||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||||
Db     1081 TGYACNAARGTNACNATGGAYAAYTTYYTNACNGCNCAYCAYGARATGGGNCAYATHCAR 1140
```

```
Qy    381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
          |||||||||||||||||   |||||||||           ||||||||||||||||||||
Db   1141 TAYGAYATGGCNTAYGCNMGNCARCCNTTYYTNYTNMGNAAYGGNGCNAAYGARGGNTTY 1200

Qy    401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
          ||||||||||||||||||||||||            ||||||||||||||||| |||
Db   1201 CAYGARGCNGTNGGNGARATHATGWSNYTNWSNGCNGCNACNCCNAARCAYYTNAARWSN 1260

Qy    421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
          |||||            ||||||||||||||  |||||||||||||||||
Db   1261 ATHGGNYTNYTNCCNWSNGAYTTYCARGARGAYWSNGARACNGARATHAAYTTYYTNYTN 1320

Qy    441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
          |||||||||   |||||||||||||||   |||||||||||||||    |||||||||
Db   1321 AARCARGCNYTNACNATHGTNGGNACNYTNCCNTTYACNTAYATGYTNGARAARTGGMGN 1380

Qy    461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
          ||||||||||||   ||||||||||||||:::||||||||||||||||||||||||||||
Db   1381 TGGATGGTNTTYMGNGGNGARATHCCNAARGARCARTGGATGAAARAARTGGTGGGARATG 1440

Qy    481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
          |||   ||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db   1441 AARMGNGARATHGTNGGNGTNGTNGARCCNYTNCCNCAYGAYGARACNTAYTGYGAYCCN 1500

Qy    501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
          |||      |||||||||   |||||||||   ||||||   |||||||||   |||:::
Db   1501 GCNWSNYTNTTYCAYGTNWSNAAYGAYTAYWSNTTYATHMGNTAYTAYACNMGNACNATH 1560

Qy    521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
          ||||||||||||||||||||||||   |||||||||||||||:::   |||      |||
Db   1561 TAYCARTTYCARTTYCARGARGCNYTNTGYCARGCNGCNAARTAYAAYGGNWSNYTNCAY 1620

Qy    541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
          ||||||||||||   |||   ||||||||||||||||||         |||
Db   1621 AARTGYGAYATHWSNAAYWSNACNGARGCNGGNCARAARYTNYTNAARATGYTNWSNYTN 1680

Qy    561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
          |||      |||||||||||||   |||   |||||||||||||||||   ||||||:::
Db   1681 GGNAAYWSNGARCCNTGGACNAARGCNYTNGARAAYGTNGTNGGNGCNMGNAAYATGGAY 1740

Qy    581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
          |||:::|||   |||||||||:::|||   |||   |||   |||:::||||||
Db   1741 GTNAARCCNYTNYTNAAYTAYTTYCARCCNYTNTTYGAYTGGYTNAARGARCARAAYMGN 1800

Qy    601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
          |||   ||||||||||||:::|||:::|||   |||||||||||||||   |||||||||
Db   1801 AAYWSNTTYGTNGGNTGGAAYACNGARTGGWSNCCNTAYGCNGAYCARWSNATHAARGTN 1860

Qy    621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
             |||   |||   |||   |||   ||||||||||||   :::|||||||||
Db   1861 MGNATHWSNYTNAARWSNGCNYTNGGNGCNAAYGCNTAYGARTGGACNAAYAAYGARATG 1920

Qy    641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
          :::   |||      |||||||||||||||   :::||||||      :::||||||
Db   1921 TTYYTNTTYMGNWSNWSNGTNGCNTAYGCNATGMGNAARTAYTTYWSNATHATHAARAAY 1980

Qy    661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
          |||   :::   |||   ||||||||||||   |||   :::   ||||||   :::
Db   1981 CARACNGTNCCNTTYYTNGARGARGAYGTNMGNGTNWSNGAYYTNAARCCNMGNGTNWSN 2040

Qy    681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
          |||   ||||||||||||   |||:::||||||   |||:::||||||      ||||||
Db   2041 TTYTAYTTYTTYGTNACNWSNCCNCARAAYGTNWSNGAYGTNATHCCNMGNWSNGARGTN 2100

Qy    701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
          |||   ||||||   |||               |||||||||   |||      |||||||||
Db   2101 GARGAYGCNATHMGNATGWSNMGNGGNMGNATHAAYGAYGTNTTYGGNYTNAAYGAYAAY 2160

Qy    721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
                ||||||   ||||||   ||||||   ||||||||||||:::
Db   2161 WSNYTNGARTTYYTNGGNATHCAYCCNACNYTNGARCCNCCNTAYCARCCNCCNGTNACN 2220

Qy    741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
          ||||||   |||:::|||||||||||||||      :::||||||||||||:::|||
Db   2221 ATHTGGYTNATHATHTTYGGNGTNGTNATGGCNYTNGTNGTNGTNGGNATHATHATHYTN 2280

Qy    761 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780
          |||   |||||||||:::      ||||||||||||:::   :::      |||||||||
Db   2281 ATHGTNACNGGNATHAARGGNMGNAARAARAARAAYGARACNAARMGNGARGARAAYCCN 2340

Qy    781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
          |||      :::||||||   |||||||||   |||   |||||||||||   ||||||
Db   2341 TAYGAYWSNATGGAYATHGGNAARGGNGARWSNAAYGCNGGNTTYCARAAYWSNGAYGAY 2400

Qy    801 ValGlnThrSerPhe 805
             ||||||   |||
Db   2401 GCNCARACNWSNTTY 2415
```

RESULT 14
AAQ10328

```
ID   AAQ10328 standard; DNA; 2477 BP.
XX
AC   AAQ10328;
XX
DT   10-APR-1991  (first entry)
XX
DE   Encodes human testicular angiotensin conversion enzyme.
XX
KW   human testicular angiotensin conversion enzyme; tACE;
KW   male sterility; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             29..2227
FT                   /*tag=  a
FT                   /product= human tACE
FT   Peptide         29..91
FT                   /*tag=  b
FT                   /label= signal peptide
XX
PN   WO9100354-A.
XX
PD   10-JAN-1991.
XX
PF   05-JUL-1990;   90WO-FR00513.
XX
PR   05-JUL-1989;   89FR-0009062.
XX
PA   (INRM ) INST NAT SANTE RECH.
XX
PI   Soubrier F,  Alhenc-Gelas F,  Hubert C,  Corvol P;
XX
DR   WPI; 1991-036748/05.
DR   P-PSDB; AAR10426.
XX
PT   Nucleic acid - encoding human testicular angiotensin conversion
PT   enzyme, used e.g. for in vitro detection of enzyme in organism
XX
PS   Claim 1; Fig 1; 48pp; French.
XX
CC   A bank of human testicular cDNA in Lambda gt11 was screened with a
CC   probe containing the final 3248 nucleotides of endothelial ACE. The
CC   complete sequence of tACE was reconstructed from 4 separate clones.
CC   It encodes a 711 amino acid mature protein and a 21 residue signal
CC   peptide. The 228-2224 sequence is identical to the 1944-3940 region
CC   of endothelial ACE. The isolated nucleic acid sequence is inserted
CC   into a plasmid for expression of polypeptides. The invention also
CC   covers parts of the sequence comprising all or part of the 29-229
CC   sequence, any sequence differing from tACE only by silent
CC   substitutions and nucleic acids which hybridise to tACE.
XX
SQ   Sequence 2477 BP; 536 A; 811 C; 695 G; 435 T; 0 other;

Alignment Scores:
Pred. No.:            6.37e-121       Length:        2477
```

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Score:                      1344.00     Matches:        259
Percent Similarity:         60.97%      Conservative:   119
Best Local Similarity:      41.77%      Mismatches:     204
Query Match:                31.32%      Indels:         38
DB:                         12          Gaps:           10

US-09-635-501-2 (1-805) x AAQ10328 (1-2477)

Qy     15 ThrAlaAlaGlnSer-----------ThrIleGluGluGlnAlaLysThrPheLeuAsp 30
Db    209 ACATCAGCCCAGAGCCCAAACCTGGTGACTGATGAGGCTGAGGCCAGCAAGTTTGTGGAG 268

Qy     31 LysPheAsnHisGluAlaGluAspLeuPheTyrGlnSerSerLeuAlaSerTrpAsnTyr 50
Db    269 GAATATGACCGGACATCCCAGGTGGTGTGGAACGAGTATGCCGAGGCCAACTGGAACTAC 328

Qy     51 AsnThrAsnIleThrGluGlu----------------------AsnValGlnAsnMet 62
Db    329 AACACCAACATCACCACAGAGACCAGCAAGATTCTGCTGCAGAAGAACATGCAAATAGCC 388

Qy     63 AsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAlaGlnMet 82
Db    389 AACCACACC-----------------------CTGAAGTACGGCACCCAGGCCAGGAAG 424

Qy     83 TyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeuGlnGln 102
Db    425 TTTGATGTGAACCAGTTGCAGAACACCACTATCAAGCGGATCATAAAGAAGGTTCAGGAC 484

Qy    103 AsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeuAsnThr 122
Db    485 CTAGAACGGGCAGCGCTGCCTGCCCAGGAGCTGGAGGAGTACAACAAGATCCTGTTGGAT 544

Qy    123 MetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGluCysLeu 142
Db    545 ATGGAAACCACCTACAGCGTGGCCACTGTGTGCCACCCGAATGGC------AGCTGCCTG 598

Qy    143 LeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgLeu 162
Db    599 CAGCTCGAGCCAGATCTGACGAATGTGATGGCCACATCCCGGAAATATGAAGACCTGTTA 658

Qy    163 TrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluGlu 182
Db    659 TGGGCATGGGAGGGCTGGCGAGACAAGGCGGGGAGAGCCATCCTCCAGTTTTACCCGAAA 718

Qy    183 TyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyr 202
Db    719 TACGTGGAACTCATCAACCAGGCTGCCCGGCTCAATGGCTATGTAGATGCAGGGGACTCG 778

Qy    203 TrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGlnLeu 222
Db    779 TGGAGGTCTATGTACGAGACACCATCCCTGGAG-------------------------- 811

Qy    223 IleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeuHisAla 242
Db    812 ---CAAGACCTGGAGCGGCTCTTCCAGGAGCTGCAGCCACTCTACCTCAACCTGCATGCC 868

Qy    243 TyrValArgAlaLysLeuMetAsnAlaTyr---ProSerTyrIleSerProIleGlyCys 261
Db    869 TACGTGCGCCGGGCCCTGCACCGTCACTACGGGGCCCAGCACATCAACCTGGAGGGGCCC 928

Qy    262 LeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSerLeu 281
Db    929 ATTCCTGCTCACCTGCTGGGGAACATGTGGGCGCAGACCTGGTCCAACATCTATGACTTG 988

Qy    282 ThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGlnAla 301
Db    989 GTGGTGCCCTTCCCTTCAGCCCCCTCGATGGACACCACAGAGGCTATGCTAAAGCAGGGC 1048

Qy    302 TrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeuPro 321
Db   1049 TGGACGCCCAGGAGGATGTTTAAGGAGGCTGATGATTTCTTCACCTCCCTGGGGCTGCTG 1108

Qy    322 AsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGlnLys 341
Db   1109 CCCGTGCCTCCTGAGTTCTGGAACAAGTCGATGCTGGAGAAGCCAACCGACGGGCGGGAG 1168

Qy    342 AlaValCysHisProThrAlaTrpAspLeuGlyLysGly---AspPheArgIleLeuMet 360
Db   1169 GTGGTCTGCCACGCCTCGGCCTGGGACTTCTACAACGGCAAGGACTTCCGGATCAAGCAG 1228

Qy    361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380
Db   1229 TGCACCACCGTGAACTTGGAGGACCTGGTGGTGGCCCACCACGAAATGGGCCACATCCAG 1288

Qy    381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400
Db   1289 TATTTCATGCAGTACAAAGACTTACCTGTGGCCTTGAGGGAGGGTGCCAACCCCGGCTTC 1348

Qy    401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420
Db   1349 CATGAGGCCATTGGGGACGTGCTAGCCCTCTCAGTGTCTACGCCCAAGCACCTGCACAGT 1408

Qy    421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440
Db   1409 CTCAACCTGCTGAGCAGTGAGGGTGGCAGCGAC---GAGCATGACATCAACTTTCTGATG 1465

Qy    441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
Db   1466 AAGATGGCCCTTGACAAGATCGCCTTTATCCCCTTCAGCTACCTCGTCGATCAGTGGCGC 1525

Qy    461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
Db   1526 TGGAGGGTATTTGATGGAAGCATCACCAAGGAGAACTATAACCAGGAGTGGTGGAGCCTC 1585

Qy    481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500
Db   1586 AGGCTGAAGTACCAGGGCCTCTGCCCCCCAGTGCCCAGGACTCAAGGTGACTTTGACCCA 1645

Qy    501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
Db   1646 GGGGCCAAGTTCCACATTCCTTCTAGCGTGCCTTACATCAGGTACTTTGTCAGCTTCATC 1705

Qy    521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
Db   1706 ATCCAGTTCCAGTTCCACGAGGCACTGTGCCAGGCAGCTGGCCACACGGGCCCCCTGCAC 1765

Qy    541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560
Db   1766 AAGTGTGACATCTACCAGTCCAAGGAGGCCGGGCAGCGCCTGGCGACCGCCATGAAGCTG 1825

Qy    561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580
Db   1826 GGCTTCAGTAGGCCGTGGCCGGAAGCCATGCAGCTGATCACGGGCCAGCCCAACATGAGC 1885

Qy    581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
Db   1886 GCCTCGGCCATGTTGAGCTACTTCAAGCCGCTGCTGGACTGGCTCCGCACGGAGAACGAG 1945

Qy    601 ------AsnSerPheValGlyTrp---SerThrAspTrpSerProTyrAlaAspGlnSer 617
Db   1946 CTGCATGGGGAGAAGCTGGGCTGGCCGCAGTACAACTGGACGCCGAACTCCGCTCGCTCA 2005

RESULT 15
AAA38330
ID   AAA38330 standard; DNA; 4020 BP.
XX
AC   AAA38330;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human angiotensin-converting enzyme (ACE) coding region.
XX
KW   Angiotensin-converting enzyme gene; ACE; coding region; polymorphism;
KW   polymorphic marker; cardiovascular disease; myocardial infarction;
KW   unstable angina; hypertension; atherosclerosis; stroke; prognosis;
KW   drug screening; treatment outcome; human; ds.
```

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XX
OS   Homo sapiens.
XX
PN   WO200022166-A2.
XX
PD   20-APR-2000.
XX
PF   13-OCT-1999;   99WO-IB01678.
XX
PR   14-OCT-1998;   98US-0104286.
PR   14-OCT-1998;   98US-0104302.
XX
PA   (EURO-) EURONA MEDICAL AB.
XX
PI   Norberg LT,  Andersson MK,  Lindstrom PHR,  Jonsson L;
XX
DR   WPI; 2000-318010/27.
XX
PT   Assessing cardiovascular status in humans involves comparing test
PT   polymorphic pattern comprising polymorphic positions within genes
PT   encoding specific proteins, with reference polymorphic pattern  -
XX
PS   Disclosure; Page 114-115; 126pp; English.
XX
CC   The invention relates to a novel method of assessing the cardiovascular
CC   status in an individual and to newly identified polymorphisms in the
CC   genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC   receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC   aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC   receptors 1 and 2. The method comprises determining the sequence at one
CC   or more polymorphic positions within these genes, and comparing the
CC   pattern of polymorphisms from the individual with a reference polymorphic
CC   pattern obtained from a population of individuals exhibiting a
CC   predetermined cardiovascular disease status. The polymorphic markers are
CC   useful for determining the predisposition of an individual to
CC   cardiovascular disorders such as myocardial infarction, unstable angina,
CC   hypertension, atherosclerosis and stroke. They are also useful for
CC   predicting the likely cardiovascular status of a patient given a
CC   treatment regimen comprising administration of cardiovascular drugs
CC   (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC   blockers) or calcium channel blockers). One or more polymorphic markers
CC   provides a basis for predicting the outcome of a treatment regimen.
CC   Fragments of the genes comprising a polymorphic site may be used as
CC   primers and probes for detecting genetic polymorphisms or in molecular
CC   library arrays for high throughput screening. The genes, and the proteins
CC   they encode are useful in the screening of potential cardiovascular
CC   drugs. Determination of an individual's polymorphic pattern reduces or
CC   eliminates trial and error in selecting a treatment for a particular
CC   individual cardiovascular patient. It also provides the ability to
CC   eliminate patients from clinical trials who are predicted to be
CC   non-responsive, or at a risk for an adverse response, to a particular
CC   treatment regimen. Adverse results in an early trial can be evaluated to
CC   identify polymorphic patterns so that the adverse results can be
CC   correlated with a sub-population of the test population, permitting
CC   exclusion of such sub-populations from the treatment group. Beneficial
CC   drugs can be approved for use in the appropriate population, thereby
CC   decreasing the number of patients required for a clinical trial, which in
CC   turn decreases the duration and cost of such trials. Sequences A38328 and
CC   A38330 represent, respectively, intron 16 and the coding region of
CC   the human ACE gene (GenBank X62855, J04144). The polymorphic sites
CC   identified are 375A/C, 582C/T, 731A/G, 1060G/A, 1215C/T, 2193G/A,
CC   2328A/G, 2741G/T, 3132C/T, 3387T/C, 3503G/C, 3906G/A; and a deletion of
CC   nucleotides 1451-1783 in intron 16.
XX
SQ   Sequence 4020 BP; 857 A; 1261 C; 1174 G; 728 T; 0 other;

Alignment Scores:
Pred. No.:              6.14e-120    Length:         4020
Score:                  1337.00      Matches:        255
Percent Similarity:     61.05%       Conservative:   118
Best Local Similarity:  41.73%       Mismatches:     204
Query Match:            31.16%       Indels:         34
DB:                     21           Gaps:           9
```

```
US-09-635-501-2 (1-805) x AAA38330 (1-4020)

Qy     20 ThrIleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeu 39
          |||   |||   :::|||    |||:::::::::::::::      ::::::   :::
Db   1952 ACTGATGAGGCTGAGGCCAGCAAGTTTGTGGAGGAATATGACCGGACATCCCAGGTGGTG 2011

Qy     40 PheTyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGlu------ 57
          :::   :::   :::   |||:::||||||||||||||||||||||||      |||
Db   2012 TGGAACGAGTATGCCGAGGCCAACTGGAACTACAACACCAACATCACCACAGAGACCAGC 2071

Qy     58 -----------------AsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSerAla 71
                           |||:::|||      |||:::
Db   2072 AAGATTCTGCTGCAGAAGAACATGCAAATAGCCAACCACACC----------------- 2113

Qy     72 PheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsnLeu 91
                :::      |||  |||:::   :::   :::   ::::::||||||
Db   2114 ------CTGAAGTACGGCACCCAGGCCAGGAAGTTTGATGTGAACCAGTTGCAGAACACC 2167

Qy     92 ThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGluAsp 111
          |||:::|||      ::::::   :::|||             :::   |||
Db   2168 ACTATCAAGCGGATCATAAAGAAGGTTCAGGACCTAGAACGGGCAGCGCTGCCTGCCCAG 2227

Qy    112 LysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGlyLys 131
          :::   :::         |||   |||   ||||||         |||   |||   ||||||
Db   2228 GAGCTGGAGGAGTACAACAAGATCCTGTTGGATATGGAAACCACCTACAGCGTGGCCACT 2287

Qy    132 ValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGluIle 151
          ||||||:::|||:::         ||||||   |||||||||   |||      :::
Db   2288 GTGTGCCACCCGAATGGC------AGCTGCCTGCAGCTCGAGCCAGATCTGACGAATGTG 2341

Qy    152 MetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171
          ||||||   |||      |||   :::   |||||||||||||||   ||||||   :::
Db   2342 ATGGCCACATCCCGGAAATATGAAGACCTGTTATGGGCATGGGAGGGCTGGCGAGACAAG 2401

Qy    172 ValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMetAla 191
             |||:::   :::         |||   :::||||||   |||   |||:::   |||
Db   2402 GCGGGGAGAGCCATCCTCCAGTTTTACCCGAAATACGTGGAACTCATCAACCAGGCTGCC 2461

Qy    192 ArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsnGly 211
          |||   |||   |||   |||   ||||||   ||||||         ||||||
Db   2462 CGGCTCAATGGCTATGTAGATGCAGGGGACTCGTGGAGGTCTATGTACGAGACACCATCC 2521

Qy    212 ValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGlu 231
          ::::::                              :::|||:::|||      |||:::
Db   2522 CTGGAG----------------------------CAAGACCTGGAGCGGCTCTTCCAG 2551

Qy    232 GluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAla 251
          |||::::::|||||||||   :::||||||||||||||||||         |||
Db   2552 GAGCTGCAGCCACTCTACCTCAACCTGCATGCCTACGTGCGCCGGGCCCTGCACCGTCAC 2611

Qy    252 Tyr---ProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMet 270
          |||         :::|||:::      |||   :::||||||||||||||||||:::|||
Db   2612 TACGGGGCCCAGCACATCAACCTGGAGGGGCCCATTCCTGCTCACCTGCTGGGGAACATG 2671

Qy    271 TrpGlyArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsn 290
          |||   :::   |||:::|||:::|||   |||   |||||||||         |||:::
Db   2672 TGGGCGCAGACCTGGTCCAACATCTATGACTTGGTGGTGCCCTTCCCTTCAGCCCCCTCG 2731

Qy    291 IleAspValThrAspAlaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGlu 310
          :::|||   |||:::||||||:::   |||   |||         :::|||:::|||||||||
Db   2732 ATGGACACCACAGAGGCTATGCTAAAGCAGGGCTGGACGCCCAGGAGGATGTTTAAGGAG 2791

Qy    311 AlaGluLysPhePheValSerValGlyLeuProAsnMetThrGlnGlyPheTrpGluAsn 330
          |||:::   ||||||   |||:::||||||         :::         ||||||
Db   2792 GCTGATGATTTCTTCACCTCCCTGGGGCTGCTGCCCGTGCCTCCTGAGTTCTGGAACAAG 2851

Qy    331 SerMetLeuThrAspProGlyAsnValGlnLysAlaValCysHisProThrAlaTrpAsp 350
          |||||||||      |||   :::   ::::::   |||||||||   :::|||||||||
Db   2852 TCGATGCTGGAGAAGCCAACCGACGGGCGGGAGGTGGTCTGCCACGCCTCGGCCTGGGAC 2911

Qy    351 LeuGlyLysGly---AspPheArgIleLeuMetCysThrLysValThrMetAspAspPhe 369
                |||   ||||||||||||      ||||||   |||   ::::::|||
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Db   2912 TTCTACAACGGCAAGGACTTCCGGATCAAGCAGTGCACCACCGTGAACTTGGAGGACCTG 2971

Qy    370 LeuThrAlaHisHisGluMetGlyHisIleGlnTyrAspMetAlaTyrAlaAlaGlnPro 389
          :::  ||||||||||||||||||||||||||||||   |||   |||           |||
Db   2972 GTGGTGGCCCACCACGAAATGGGCCACATCCAGTATTTCATGCAGTACAAAGACTTACCT 3031

Qy    390 PheLeuLeuArgAsnGlyAlaAsnGluGlyPheHisGluAlaValGlyGluIleMetSer 409
             ||||||   |||||||||   ||||||||||||||:::|||::::::::::::
Db   3032 GTGGCCTTGAGGGAGGGTGCCAACCCCGGCTTCCATGAGGCCATTGGGGACGTGCTAGCC 3091

Qy    410 LeuSerAlaAlaThrProLysHisLeuLysSerIleGlyLeuLeuSerProAspPheGln 429
          ||||||    :::|||||||||||||||   |||:::   |||||||||    :::
Db   3092 CTCTCAGTGTCTACGCCCAAGCACCTGCACAGTCTCAACCTGCTGAGCAGTGAGGGTGGC 3151

Qy    430 GluAspAsnGluThrGluIleAsnPheLeuLeuLysGlnAlaLeuThrIleValGlyThr 449
             |||   |||   :::||||||||||||:::|||   ||||||      :::
Db   3152 AGCGAC---GAGCATGACATCAACTTTCTGATGAAGATGGCCCTTGACAAGATCGCCTTT 3208

Qy    450 LeuProPheThrTyrMetLeuGluLysTrpArgTrpMetValPheLysGlyGluIlePro 469
          :::||||||:::|||::::::::::::|||||||||   ||||||   |||   |||
Db   3209 ATCCCCTTCAGCTACCTCGTCGATCAGTGGCGCTGGAGGGTATTTGATGGAAGCATCACC 3268

Qy    470 LysAspGlnTrpMetLysLysTrpTrpGluMetLysArgGluIleValGlyValValGlu 489
          |||:::   :::   ::::::||||||   ::::::   :::      |||:::
Db   3269 AAGGAGAACTATAACCAGGAGTGGTGGAGCCTCAGGCTGAAGTACCAGGGCCTCTGCCCC 3328

Qy    490 ProValProHisAspGluThrTyrCysAspProAlaSerLeuPheHisValSerAsnAsp 509
          |||||||||      :::         ||||||   :::   |||||||:::   :::
Db   3329 CCAGTGCCCAGGACTCAAGGTGACTTTGACCCAGGGGCCAAGTTCCACATTCCTTCTAGC 3388

Qy    510 TyrSerPheIleArgTyrTyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeu 529
                :::||||||||||:::         :::   ||||||||||||   |||||||||
Db   3389 GTGCCTTACATCAGGTACTTTGTCAGCTTCATCATCCAGTTCCAGTTCCACGAGGCACTG 3448

Qy    530 CysGlnAlaAlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGlu 549
          ||||||||||||   |||   ||||||||||||||||||||||||         |||   |||
Db   3449 TGCCAGGCAGCTGGCCACACGGGCCCCCTGCACAAGTGTGACATCTACCAGTCCAAGGAG 3508

Qy    550 AlaGlyGlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAla 569
          ||||||||||:::|||            ::::::||||||   |||   ||||||      |||
Db   3509 GCCGGGCAGCGCCTGGCGACCGCCATGAAGCTGGGCTTCAGTAGGCCGTGGCCGGAAGCC 3568

Qy    570 LeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGlu 589
          ::::::   :::   |||      ||||||:::         :::|||:::|||||||:::
Db   3569 ATGCAGCTGATCACGGGCCAGCCCAACATGAGCGCCTCGGCCATGTTGAGCTACTTCAAG 3628

Qy    590 ProLeuPheThrTrpLeuLysAspGlnAsnLys------AsnSerPheValGlyTrp--- 606
          ||||||      |||||||:::   :::|||:::                :::|||||||
Db   3629 CCGCTGCTGGACTGGCTCCGCACGGAGAACGAGCTGCATGGGGAGAAGCTGGGCTGGCCG 3688

Qy    607 SerThrAspTrpSerProTyrAlaAspGlnSer 617
                :::|||:::|||   :::   :::|||
Db   3689 CAGTACAACTGGACGCCGAACTCCGCTCGCTCA 3721
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Search completed: October 9, 2002, 18:07:43
Job time : 295 secs